

SEARCH REQUEST FORM

Scientific and Technical Information Center

Requester's Full Name: _____ Examiner #: _____ Date: _____
 Art Unit: _____ Phone Number 30 _____ Serial Number: _____
 Mail Box and Bldg/Room Location: _____ Results Format Preferred (circle): PAPER DISK E-MAIL

If more than one search is submitted, please prioritize searches in order of need.

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc. if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: _____

Inventors (please provide full names): _____

Earliest Priority Filing Date: _____

**For Sequence Searches Only* Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.*

STAFF USE ONLY

	Type of Search	Vendors and cost where applicable
Searcher: _____	NA Sequence (#) _____	STN _____
Searcher Phone #: if Contact: 308-4499 Sheppard	AA Sequence (#) _____	Dialog _____
Searcher Location: _____	Structure (#) _____	Questel/Orbit _____
Date Searcher Picked Up: 8/8/01	Bibliographic _____	Dr.Link _____
Date Completed: _____	Litigation _____	Lexis/Nexis _____
Searcher Prep & Review Time: _____	Fulltext _____	Sequence Systems _____
Clerical Prep Time: _____	Patent Family _____	WWW/Internet _____
Online Time: _____	Other _____	Other (specify) _____

L3 ANSWER 1 OF 5 CAPLUS COPYRIGHT 2003 ACS
 AN 2003:117556 CAPLUS
 TI Method for treating diabetes and obesity with fibroblast growth factor 21
 IN Glasebrook, Andrew Lawrence; Hammond, Lisa Janine; Kharitononkov, Alexei;
 Shiyanova, Tatiyana Leonidovna
 PA Eli Lilly and Company, USA
 SO PCT Int. Appl., 32 pp.
 CODEN: PIXXD2

DT Patent
 LA English

FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 2003011213	A2	20030213	WO 2002-US21290	20020722
	W:	AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM			
	RW:	GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG			
PRAI	US 2001-308702P	P	20010730		
	US 2002-347991P	P	20020110		
AB	A method for treating diabetes and obesity comprises administering an effective amt. of fibroblast growth factor 21. FGF-21 stimulated glucose uptake in a mouse obesity model and reduced plasma glucose levels in a dose-dependent manner in fat, diabetic ZDF rats. FGF-21 did not induce hypoglycemia in lean ZDF rats.				

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 6, 2001, 20:58:04 ; Search time 1964.36 Seconds
(without alignments)
5726.494 Million cell updates/sec

Title: US-09-391-861-1
Perfect score: 1190
Sequence: 1 gaggatccagccgaagagg.....aaaaaaaaaaaaaaaaaaaa 1190

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 10228115 seqs, 4726426750 residues 20456230
Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*

1:	gb_est1:*
2:	gb_est2:*
3:	gb_est3:*
4:	gb_est4:*
5:	gb_est5:*
6:	gb_est6:*
7:	gb_est7:*
8:	gb_est8:*
9:	gb_est9:*
10:	gb_est10:*
11:	gb_est11:*
12:	gb_est12:*
13:	gb_est13:*
14:	gb_est14:*
15:	gb_est15:*
16:	gb_est16:*
17:	gb_est17:*
18:	gb_est18:*
19:	gb_est19:*
20:	gb_est20:*
21:	gb_est21:*
22:	gb_est22:*
23:	gb_est23:*
24:	gb_est24:*
25:	gb_est25:*
26:	gb_est26:*
27:	gb_est27:*
28:	gb_est28:*
29:	gb_est29:*
30:	gb_est30:*
31:	gb_est31:*
32:	gb_est32:*
33:	gb_est33:*
34:	gb_est34:*
35:	gb_est35:*
36:	gb_est36:*
37:	gb_est37:*
38:	gb_est38:*
39:	gb_est39:*
40:	gb_est40:*
41:	gb_est41:*
42:	gb_est42:*
43:	gb_est43:*
44:	gb_est44:*
45:	gb_est45:*
46:	gb_est46:*
47:	gb_est47:*
48:	gb_est48:*
49:	gb_est49:*
50:	gb_est50:*
51:	gb_est51:*
52:	gb_est52:*
53:	gb_est53:*
54:	gb_est54:*
55:	gb_est55:*
56:	gb_est56:*
57:	gb_est57:*
58:	gb_est58:*
59:	gb_est59:*
60:	gb_est60:*
61:	gb_est61:*
62:	gb_est62:*
63:	gb_est63:*
64:	gb_est64:*
65:	gb_est65:*
66:	gb_est66:*
67:	gb_est67:*
68:	gb_est68:*
69:	gb_est69:*
70:	gb_est70:*
71:	gb_est71:*
72:	gb_est72:*
73:	gb_est73:*
74:	gb_est74:*
75:	gb_est75:*
76:	gb_est76:*
77:	gb_est77:*
78:	gb_est78:*
79:	gb_est79:*
80:	gb_est80:*
81:	gb_est81:*
82:	gb_est82:*
83:	gb_est83:*
84:	gb_est84:*
85:	gb_est85:*
86:	gb_est86:*
87:	gb_est87:*
88:	gb_est88:*
89:	gb_est89:*
90:	gb_est90:*
91:	gb_est91:*
92:	gb_est92:*
93:	gb_est93:*
94:	gb_est94:*
95:	gb_est95:*
96:	gb_est96:*
97:	gb_est97:*
98:	gb_est98:*
99:	gb_est99:*
100:	gb_est100:*
101:	gb_est101:*
102:	gb_est102:*
103:	gb_est103:*
104:	gb_est104:*
105:	gb_est105:*
106:	gb_est106:*
107:	gb_est107:*
108:	gb_est108:*
109:	gb_est109:*
110:	gb_est110:*
111:	gb_est111:*
112:	gb_est112:*
113:	gb_est113:*
114:	gb_est114:*
115:	gb_est115:*
116:	gb_est116:*

117: gb_est48:*
118: gb_est49:*
119: gb_est50:*
120: gb_est51:*
121: gb_est52:*
122: gb_est53:*
123: gb_est54:*
124: gb_est55:*
125: gb_est56:*
126: gb_est57:*
127: gb_est58:*
128: gb_est59:*
129: gb_est60:*
130: gb_est61:*
131: gb_est62:*
132: gb_est63:*
133: gb_est64:*
134: gb_est65:*
135: gb_est66:*
136: gb_est67:*
137: gb_est68:*
138: gb_est69:*
139: gb_est70:*
140: gb_est71:*
141: gb_est72:*
142: gb_est73:*
143: gb_est74:*
144: gb_est75:*
145: gb_est76:*
146: gb_est77:*
147: gb_est78:*
148: gb_est79:*
149: gb_est80:*
150: gb_est81:*
151: gb_est82:*
152: gb_est83:*
153: gb_est84:*
154: gb_est85:*
155: gb_est86:*
156: gb_est87:*
157: gb_est88:*
158: gb_est89:*
159: gb_est90:*
160: gb_est91:*
161: gb_est92:*
162: gb_est93:*
163: gb_est94:*
164: gb_est95:*
165: gb_est96:*
166: gb_est97:*
167: gb_est98:*
168: gb_est99:*
169: gb_est100:*
170: gb_est101:*
171: gb_est102:*
172: gb_est103:*
173: gb_est104:*
174: gb_est105:*
175: gb_est106:*
176: gb_est107:*
177: gb_est108:*
178: gb_est109:*
179: gb_est110:*
180: gb_est111:*
181: gb_est112:*
182: gb_est113:*
183: gb_est114:*
184: gb_est115:*
185: gb_est116:*
186: gb_est117:*
187: gb_est118:*
188: gb_est119:*
189: gb_est120:*

190: gb_est121:*
191: gb_est122:*
192: gb_est123:*
193: gb_est124:*
194: gb_est125:*
195: gb_est126:*
196: gb_est127:*
197: gb_est128:*
198: gb_est129:*
199: gb_est130:*
200: gb_est131:*
201: gb_est132:*
202: gb_est133:*
203: gb_est134:*
204: gb_est135:*
205: gb_est136:*
206: gb_est137:*
207: gb_est138:*
208: gb_est139:*
209: gb_est140:*
210: gb_est141:*
211: gb_est142:*
212: gb_est143:*
213: gb_est144:*
214: gb_est145:*
215: gb_est146:*
216: gb_est147:*
217: gb_est148:*
218: gb_est149:*
219: gb_est150:*
220: gb_est151:*
221: gb_est152:*
222: gb_est153:*
223: gb_est154:*
224: gb_est155:*
225: gb_est156:*
226: gb_est157:*
227: gb_est158:*
228: gb_est159:*
229: gb_est160:*
230: gb_est161:*
231: gb_est162:*
232: gb_est163:*
233: gb_est164:*
234: gb_est165:*
235: gb_est166:*
236: gb_est167:*
237: gb_est168:*
238: gb_est169:*
239: gb_est170:*
240: gb_est171:*
241: gb_est172:*
242: gb_est173:*
243: gb_est174:*
244: gb_est175:*
245: gb_est176:*
246: gb_est177:*
247: gb_est178:*
248: gb_est179:*
249: gb_est180:*
250: gb_est181:*
251: gb_est182:*
252: gb_est183:*
253: gb_est184:*
254: gb_est185:*
255: gb_est186:*
256: gb_est187:*
257: gb_est188:*
258: gb_est189:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.


```
/note="putative"
/codon_start=1
/protein_id="BAB25115.1"
/db_xref="GI:12841203"
/translation="MEMMRKRVGTLGLWVRLLLAVFLVGYQAYPIPDSSPLQLFGGQ
VRQSLVTDQDDQDFEAHLREIDGTVVGAARHPESLLELKALKPGVIOILGVKASRF
LCQDFDALVGSHPEDPEACSFRELLLEDGYNVYQSEAHGLPLRLPKDPSNQDATSW
GPVFLPMPGLLLHPDQAGFLPPEPPGVSSDPLSMVEPLQGRSFYAS"
BASE COUNT      204 a      278 c      241 g      227 t
ORIGIN
Query Match      35.5%; Score 422; DB 192; Length 950;
Best Local Similarity 77.3%; Pred. No. 1.5e-63;
Matches 544; Conservative 0; Mismatches 145; Indels 15; Gaps 2;
QY 191 tcttgctgtcttctctgctggagcctgcaggcagacacccctcctcactccagtcctc 250
Db 237 TcTGTGCTGTCTTCTGCTGGGGGTCTACCAAGCATACCCCATCCTGACTCCAGCCGCC 296
QY 251 tctgcaattcggggcccaagtcctggcgcggtacctctacacagatgacccagcaga 310
Db 297 TcTCCAGTTTGGGGTCAAGTCCGCGAGGTACTCTACACAGATACGACCAAGACA 356
QY 311 cagaagccacactgagatcaggaggtggagcgtggggggcgctgctgaccagagcc 370
Db 357 CTGAAGCCACCTTGGAGATCAGGGAGGTGGAACAGTGTAGGCGCAGCACACCGCAGTC 416
QY 371 ccgaaagtctcctgcagctgaaagccttgaagccgttgaagccgggagttattcaaatctctggagtc 430
Db 417 CAGAAAGTCTCCTGGAGCTCAAAAGCCTTGAAGCCAGGGGTCAATCAAAATCCTTGGGTGTC 476
QY 431 agacatccaggttcctgtgccagcgcagatggggccctgtatgatcgctccactttg 490
Db 477 AAGCCCTTAGGTTCTTTGCGCAACAGCAGATGGAGCTCTCTATGATGCCCTCCTACTTTG 536
QY 491 accctgagcctcagcttcggagctgctctttgagagcagatataatgtttaccagt 550
Db 537 ATCCTGAGGCTCGAGTTCAGAGAACTGCTGCTGGAGGAGCGTTTACAATGTGTACCACT 596
QY 551 ccgaagccacggcctcccgctgcaactgccagggagaaagtcacacccagggaccctg 610
Db 597 CTGAAGCCCATGGCCCTGCCCTCGCTCTGCTCAGAAAGGACTCCCAAAACAGGATGCAA 656
QY 611 caccgcagagacagctcgtctctgccactaccagcctgccccccgcaccccccgagc 670
Db 657 CATCTGGGACCTGTGCGGTTCTCTGCCCATGCCAGGCTGTCTCCAGAGCCGCCCAAGACC 716
QY 671 caccggaaatcctggccccccagcccccccgatgtgggctcctcggaccctctgagcatgg 730
Db 717 AAGCAGGATTCTTGCCTCCAGAGCCGCCAGATGTGGCTCTCTGACCCCTTGAGCATGG 776
QY 731 tggagacctccagggccggaagccccagctacgcttcctga-----agccagagc 781
Db 777 TAGAGCCTTTACAGGGCGGGAAGCCGCCAGCTATGCGCTGACTCTCTCCTGAATCTAGGGC 836
QY 782 tgtttactatgacatctcctcttattattattattattattattattt-----t 835
Db 837 TGTTCCTTTTGGGTTTCCACTATTATTATACGGGTATTATCTATTATTATTATTATTAG 896
QY 836 tttattttcttacttgagataataagagttccagaggagggat 879
Db 897 TTTTTCCTCTTACTTGGAAATAATAAAGAGTCTGAAAGAAAAAT 940
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 496)
Mahairas,G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
Hood,L.
Sequence-tagged connectors: A sequence approach to mapping and
scanning the human genome
Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
99380589
Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Sequence Tagged Connector
Plate: 3207 row: O column: 17
Class: BAC ends
High quality sequence stop: 496.
Location/Qualifiers
I. .496
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="plate=3207 Col=17 Row=O"
/clone_lib="CIT Approved Human Genomic Sperm Library D"
/sex="male"
/note="Organ: sperm; Vector: pBelobAC11; BAC Clones in
E-Clon DH10B."
BASE COUNT      106 a      139 c      137 g      100 t      14 others
ORIGIN
Query Match      27.2%; Score 323.6; DB 225; Length 496;
Best Local Similarity 93.3%; Pred. No. 1.6e-46;
Matches 332; Conservative 0; Mismatches 24; Indels 0; Gaps 0;
QY 1 gagatccagccgaagaggagccagcactcagccagccactgagctgactcactcagcaga 60
Db 128 GAGGATCCAGCCGGAAGAGGAGGAGCCAGGCACCTCAGCCACCTGACTTACTCCTCGGACA 187
QY 61 actggaattctggaccaattctaaacactcagcttctccgagctcacaccgcagagatc 120
Db 188 ACTGGAATCTGGCAACCAATTCTAAACCACTCAGCTTCTCCGAGCTCACACCCCGAGATC 247
QY 121 acctgagagaccgagccattgatgactcgagcagagaccgggttcgagcactcaggagctg 180
Db 248 ACCTGANGACCCGAGCCCAATTGATGGACATCGGACGAGACCGGGTTCGAGACTCAGGGCTG 307
QY 181 tgggtttctgtgctggtgtcttctgctggagcctgcccaggccacacccatccctgac 240
Db 308 TGGGTTTCTGTGCTGGCTGGGCTTCTGTGGAGGCTGCCAGGCACACCNATCCCTGAC 367
QY 241 tccagtctctctcgaattcggggcccaagtcgcgcagcagcagctcactacacagatgat 300
Db 368 TCCAGTCTCTTCTTCANNTATCGGGGCCAAGTCCGGCAGCGGTACTCTTACACAGATGAT 427
QY 301 gccagcagacagaagccacacctggagatcagagagagatggagcgttggggggcgc 356
Db 428 GCNACGACACAGAAAGCCACCCCTGAGATCANGAGTGTATGGACTGNGNGNGTNGC 483
RESULT 3
BE785063
LOCUS BE785063 775 bp mRNA EST 20-OCT-2000
DEFINITION 60147819F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3881069 5',
mrna sequence.
ACCESSION BE785063
VERSION BE785063.1 GI:10206261
KEYWORDS EST.
```

```

SOURCE
ORGANISM      human.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS      NIH-MGC http://mgi.nci.nih.gov/.
TITLE        National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL      Unpublished (1999)
COMMENT      Contact: Robert Strausberg, Ph.D.
              Email: cgabs-r@mail.nih.gov
              Tissue Procurement: DTD/DTP/Gazdar
              cDNA Library Preparation: Life Technologies, Inc.
              cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
              DNA Sequencing by: Incyte Genomics, Inc.
              Clone distribution: MGC clone distribution information can be
              found through the I.M.A.G.E. Consortium/LNL at:
              http://image.llnl.gov
              Plate: L1AM9649 row: e column: 06
              High quality sequence stop: 694.
              Location/Qualifiers
                1..775
                  /organism="Homo sapiens"
                  /db_xref="taxon:9606"
                  /clone="IMAGE:3881069"
                  /clone_lib="NIH_MGC_68"
                  /tissue_type="large cell carcinoma"
                  /lab_host="DH10B (phage-resistant)"
                  /note="Organ: lung; Vector: pCMV-Sport6; Site_1: NotI;
                    Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
                    Average insert size 1.8 kb. Library constructed by Life
                    Technologies."
                182 a 219 c 205 g 169 t

BASE COUNT
ORIGIN
Query Match      18.5%; Score 220.2; DB 140; Length 775;
Best Local Similarity 87.3%; Pred. No. 1.2e-28;
Matches 310; Conservative 0; Mismatches 38; Indels 7; Gaps 6;

QY 1 gagatcagcgaagagagcagcactcagccactcagccactcagctcactcactcagcaga 60
DB 422 GAGGATCCAGCCGAAAGAGAGGAGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 481
QY 61 actggaatctggcaccatttaaacactcagcttctcagagctcacaccccgagat- 119
DB 482 ACTGGAATCTGGCACCACCAATTCCTAAA-CACTCAGCTTCTCGAGCTCACACCCCGAGATC 540
QY 120 cactcagcagcagcagcattgatgactcagcagcagcagcagcagcagcagcagcagcagc 179
DB 541 CACCTGAGGACCCGAGCCATTGATGGACTCGGACGAGACCGGGTTTCGAGCACTCAGGGCT 600
QY 180 gt-gggtttctgtgctgtgtcttctgtcgtgagcctcgcagcgcacacccca-tccct 237
DB 601 GTGGGTATCTGTGCTGTGTGTGTCTGTGCTGGAGCCCTGCCAGTGGAACCCCATTTCCCT 660
QY 238 gactccagtcct-ctctgcgaattcggggcccaagtcgcgagcgcagcagcagcagcagcagc 296
DB 661 GAATCCAGTCTCTCTCTCTGCAATTCGGGGGCAAGTCCCGGAGAGGAGGAGGAGGAGGAGGAG 720
QY 297 tgatgccacagacagagaagccacactggagatcagggagagatcagggagcagcagcagcagc 351
DB 721 TAATGCCCA--AAAAAGAGAGCCACCTGGAGATCAAGGCGGATTCGACACAGGGGG 773

RESULT 4
LOCUS      AV049138
DEFINITION AV049138 Mus musculus pancreas C57BL/6J adult Mus musculus cDNA
            clone 1810008N24, mRNA sequence.
ACCESSION  AV049138
VERSION     AV049138.1 GI:5134910
KEYWORDS   EST.
SOURCE     house mouse.

```

```

ORGANISM      Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
AUTHORS      Carninci, P., Shibata, K., Ozawa, Y., Konno, H., Itoh, M., Aizawa, K.,
              Akahira, S., Akiyama, J., Fukuda, S., Fukunishi, Y., Funayama, T., Hara
              , A., Hayatsu, N., Hori, F., Ishikawa, T., Itoh, M., Izawa, M., Kawai, J.,
              Kikuchi, N., Kojima, Y., Matsuyama, T., Niitsuma, H., Oda, H., Owa, C.,
              Sato, K., Shibata, Y., Shigemoto, Y., Shiraki, F., Sogabe, Y., Sugahara
              , Y., Suzuki, H., Suzuki, H., Tateo, M., Tomaru, Y., Tominaga, N.,
              Watanabe, S., Yagame, M., Yamamura, T., Yokota, T., Yoshino, M.,
              Muramatsu, M., Okazaki, Y. and Hayashizaki, Y.
              RIKEN Mouse ESTs
              Unpublished (1999)
              Contact: Chie Owa
              Genome Science Laboratory
              RIKEN
              3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
              Tel: 81-298-36-9145
              Fax: 81-298-36-9098
              Email: genome-res@rtc.riken.go.jp
              Thermolabile enzymes by
              trehalose and its application for the synthesis of full length cDNA
              (Proc. Natl. Acad. Sci. U.S.A. 95(2):520-524 (1998))
              Transcriptional sequencing: A method for DNA sequencing using RNA
              polymerase (Proc. Natl. Acad. Sci. U.S.A. 95(7):3455-3460 (1998))
              Please visit our web site (http://genome.rtc.riken.go.jp) for
              further details.
              Location/Qualifiers
                1..307
                  /organism="Mus musculus"
                  /strain="C57BL/6J"
                  /db_xref="taxon:10090"
                  /clone="1810008N24"
                  /clone_lib="Mus musculus pancreas C57BL/6J adult"
                  /sex="male"
                  /tissue_type="pancreas"
                  /dev_stage="adult"
                65 a 72 c 67 g 103 t

BASE COUNT
ORIGIN
Query Match      10.7%; Score 127; DB 109; Length 307;
Best Local Similarity 68.9%; Pred. No. 1.6e-12;
Matches 210; Conservative 0; Mismatches 80; Indels 15; Gaps 2;

QY 578 tgccagggaacaagtcccccacccgggacccctgcaccccgagcagcagcagcagcagcagcagc 637
DB 1 TGCCTTAGAAGGAATCCCAACAGGATGCAACATTCCTGGGGAGCTGTGGCTTCCTGC 60
QY 638 cactaccaggcctccccccaccccgagcagcagcagcagcagcagcagcagcagcagcagcagc 697
DB 61 CCATGGCAGGCTGATTCATGAGCCCCCAAGACCAAGCAGGATTCCTGCCCCAGAGCCCC 120
QY 698 cagatgtgggtcctcgcgacccctcgcagcctcgcagcctcgcagcctcgcagcctcgcagcctcgc 757
DB 121 CAGATGTGGATCTTTTGACCCCTTGAGCCTGTAGAGCCTTACAGGCGCGAGGCCCA 180
QY 758 gctcagcttcctga-----agccagagcgtgttactatgacatcctcttatt 808
DB 181 GCTATGCGCTCCTGATTTTCTCTGAATTTAGGCTGTTTTTTTTTTGGTTCCTCACTATT 240
QY 809 tattaggtattattcttattattt-----tttttttttttttttttttttttttttttttttttt 862
DB 241 ATTACGGGTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 300
QY 863 gagtt 867
DB 301 GAGTT 305

RESULT 5
AV050323

```

LOCUS AV050323 310 bp mRNA EST 22-JUN-1999
 DEFINITION AV050323 Mus musculus pancreas C57BL/6J adult Mus musculus CDNA
 clone 1810013H18, mRNA sequence.
 ACCESSION AV050323
 VERSION AV050323.1 GI:5136095
 KEYWORDS EST.
 SOURCE house mouse.
 ORGANISM Mus musculus.
 REFERENCE 1 (bases 1 to 310)
 AUTHORS Carninci, P., Shibata, K., Ozawa, Y., Konno, H., Itoh, M., Aizawa, K., Akahira, S., Akiyama, J., Fukuda, S., Fukunishi, Y., Funayama, T., Hara, A., Hayatsu, N., Hori, F., Ishikawa, T., Itoh, M., Izawa, M., Kawai, J., Kikuchi, N., Kojima, Y., Matsuyama, T., Niitsuma, H., Oda, H., Owa, C., Sato, K., Shibata, Y., Shigemoto, Y., Shiraki, T., Sogabe, Y., Sugahara, Y., Suzuki, H., Suzuki, H., Tateo, M., Tomaru, Y., Tominaga, N., Watanabe, S., Yagame, M., Yamamura, T., Yokota, T., Yoshino, M., Muramatsu, M., Okazaki, Y. and Hayashizaki, Y.
 TITLE RIKEN Mouse ESTs
 JOURNAL Unpublished (1999)
 COMMENT Contact: Chie Owa
 Genome Science Laboratory
 RIKEN
 3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
 Tel: 81-298-36-9145
 Fax: 81-298-36-9098
 Email: genome-res@rtc.riken.go.jp
 Thermotabilization and thermostabilization of thermolabile enzymes by trehalose and its application for the synthesis of full length cDNA (Proc. Natl. Acad. Sci. U.S.A. 95(2):520-524 (1998))
 Transcriptional sequencing: A method for DNA sequencing using RNA polymerase (Proc. Natl. Acad. Sci. U.S.A. 95(7):3455-3460 (1998))
 Please visit our web site (http://genome.rtc.riken.go.jp) for further details.

FEATURES
 source
 1. 310
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="1810013H18"
 /clone_lib="Mus musculus pancreas C57BL/6J adult"
 /sex="male"
 /tissue_type="pancreas"
 /dev_stage="adult"
 BASE COUNT 66 a 72 c 67 g 105 t
 ORIGIN

Query Match 10.4%; Score 123.2; DB 109; Length 310;
 Best Local Similarity 68.0%; Pred. No. 7.3e-12;
 Matches 208; Conservative 0; Mismatches 83; Indels 15; Gaps 2;
 QY 577 ctgcagggaacagtcacccacacgggaccctgcaccccgaggaccagctgcttcgtg 636
 Db 3 CTGCTTCAGAGAGACTCCCAACACGAGGATGCAAAATTTCTGGGGACATGTGCGATTCGTG 62
 QY 637 ccactaccaggctgcctcccccaccccgaggaccacccggaatcctggtcccccagccc 696
 Db 63 CCATGCGCAGGTTGTTCCACAGGCCCCNAGACACGAGGATTCCTGCCCCCAGAGCCC 122
 QY 697 ccgatgtgggtcctcgagaccctcgagcatgggtgggacctccacggccgaagcccc 756
 Db 123 CCAGATGTGGGTCTTTTGACCCCTGAGCATGGTAGAGCCTTTACAGGGCCGGAAGCCCC 182
 QY 757 agctaagcttctctga-----agccagaggtggttactatgacatctctcttatt 807
 Db 183 AGCATGCTCCTGGAATTTTCTCGAATTTAGGGCTGTTTTTTTGGGTTTCCACTTAAT 242
 QY 808 ttattaggttatttatttatttattt-----ttttatttttcttacttgagataataa 861
 Db 243 TATTACGGGTATTATTATTATTATTATTATTATTATTATTATTATTATTATTATTATTATT 302

QY 862 agagtt 867
 Db 303 AGAGTT 308
 RESULT 6
 AV050161 301 bp mRNA EST 22-JUN-1999
 LOCUS AV050161 Mus musculus pancreas C57BL/6J adult Mus musculus CDNA
 DEFINITION clone 1810012O18, mRNA sequence.
 ACCESSION AV050161
 VERSION AV050161.1 GI:5135933
 KEYWORDS EST.
 SOURCE house mouse.
 ORGANISM Mus musculus.
 REFERENCE 1 (bases 1 to 301)
 AUTHORS Carninci, P., Shibata, K., Ozawa, Y., Konno, H., Itoh, M., Aizawa, K., Akahira, S., Akiyama, J., Fukuda, S., Fukunishi, Y., Funayama, T., Hara, A., Hayatsu, N., Hori, F., Ishikawa, T., Itoh, M., Izawa, M., Kawai, J., Kikuchi, N., Kojima, Y., Matsuyama, T., Niitsuma, H., Oda, H., Owa, C., Sato, K., Shibata, Y., Shigemoto, Y., Shiraki, T., Sogabe, Y., Sugahara, Y., Suzuki, H., Suzuki, H., Tateo, M., Tomaru, Y., Tominaga, N., Watanabe, S., Yagame, M., Yamamura, T., Yokota, T., Yoshino, M., Muramatsu, M., Okazaki, Y. and Hayashizaki, Y.
 TITLE RIKEN Mouse ESTs
 JOURNAL Unpublished (1999)
 COMMENT Contact: Chie Owa
 Genome Science Laboratory
 RIKEN
 3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
 Tel: 81-298-36-9145
 Fax: 81-298-36-9098
 Email: genome-res@rtc.riken.go.jp
 Thermotabilization and thermostabilization of thermolabile enzymes by trehalose and its application for the synthesis of full length cDNA (Proc. Natl. Acad. Sci. U.S.A. 95(2):520-524 (1998))
 Transcriptional sequencing: A method for DNA sequencing using RNA polymerase (Proc. Natl. Acad. Sci. U.S.A. 95(7):3455-3460 (1998))
 Please visit our web site (http://genome.rtc.riken.go.jp) for further details.

FEATURES
 source
 1. 301
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="1810012O18"
 /clone_lib="Mus musculus pancreas C57BL/6J adult"
 /sex="male"
 /tissue_type="pancreas"
 /dev_stage="adult"
 BASE COUNT 63 a 70 c 65 g 103 t
 ORIGIN

Query Match 10.1%; Score 120.4; DB 109; Length 301;
 Best Local Similarity 69.7%; Pred. No. 2.2e-11;
 Matches 198; Conservative 0; Mismatches 71; Indels 15; Gaps 2;
 QY 611 caccacagagacagctcgcttctgcacatcacaggctgccccccgacacccccgagc 670
 Db 7 CATACTGGGACCTGTGCGCTTCTTGCCCATGCCAGGCTGTTCACAGAGCCCCAAGACC 66
 QY 671 caccggaatcctggccccccagcccccgatgtggctcctcgagccctctgagcatgg 730
 Db 67 AAGCAGGATTCCTGCCCCCAGAGCCCCCAGATGTGGGTCTCTTTGACCCCTCAGCATGG 126
 QY 731 tgggaccttccccagggccgaagccccagctacgcttctctga-----agccagaggc 781
 Db 127 TAGAGCCTTTTACAGGGCCGAAGCCCCAGCTATGCGTCTCTGATTTTCTCTGAATAGGGC 186
 QY 782 tgtttactatgacatctcctctttattattattattattattattttttttttttttttt 835

```

|||||
Db 187 TGTTCCTTTTGGGTTTCCACTATTATTACGGGTATTATTATTATTATTATTATTAG 246
QY 836 ttatttttcttactgagataaagaagcttccagagaggat 879
|||||
Db 247 TTTTTCCTTCTTCTGGAATAAAGAGCTCTGAAGAAAAAT 290
|||||

RESULT 7
AV052213 288 bp mRNA EST 22-JUN-1999
LOCUS AV052213 Mus musculus pancreas C57BL/6J adult Mus musculus cDNA
DEFINITION clone 1810021E04, mRNA sequence.
ACCESSION AV052213
VERSION AV052213.1 GI:5137985
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 288)
Carninci,P., Shibata,K., Ozawa,Y., Konno,H., Itoh,M., Aizawa,K.,
Akahira,S., Akiyama,J., Fukuda,S., Fukunishi,Y., Funayama,T., Hara
A., Hayatsu,N., Hori,F., Ishikawa,T., Itoh,M., Izawa,M., Kawai,J.,
Kikuchi,N., Kojima,Y., Matsuyama,T., Niitsuma,H., Oda,H., Owa,C.,
Sato,K., Shibata,Y., Shigemoto,Y., Shiraki,T., Sogabe,Y., Sugahara
Y., Suzuki,H., Suzuki,H., Tateno,M., Tomaru,Y., Tomimaga,N.,
Watanabe,S., Yagame,M., Yamamura,T., Yokota,T., Yoshino,M.,
Muramatsu,M., Okazaki,Y. and Hayashizaki,Y.
RIKEN Mouse ESTs
Unpublished (1999)
Contact: Chie Owa
Genome Science Laboratory
RIKEN
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: 81-298-36-9145
Fax: 81-298-36-9098
Email: genome-res@rtc.riken.go.jp
Thermostabilization and thermostabilization of thermolabile enzymes by
trehalose and its application for the synthesis of full length cDNA
(Proc. Natl. Acad. Sci. U.S.A. 95(2):520-524 (1998))
Transcriptional sequencing: A method for DNA sequencing using RNA
polymerase (Proc. Natl. Acad. Sci. U.S.A. 95(7):3455-3460 (1998))
Please visit our web site (http://genome.rtc.riken.go.jp) for
further details.
FEATURES
source
Location/Qualifiers
1..288
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="1810021E04"
/clone_lib="Mus musculus pancreas C57BL/6J adult"
/sex="male"
/tissue_type="pancreas"
/dev_stage="adult"
BASE COUNT 62 a 65 c 61 g 100 t
ORIGIN
Query Match 9.9%; Score 118; DB 109; Length 288;
Best Local Similarity 70.6%; Pred. No. 5.8e-11;
Matches 192; Conservative 0; Mismatches 65; Indels 15; Gaps 2;

QY 623 cagctgcttctgcactaccagcctgccccccgagccagccagccgaatcc 682
|||||
Db 1 CTGTGGCTTCTGCGCATGCCAGGCTGATCCAGAGCCCCAACAGCAGGATCC 60
|||||
QY 683 tggccccagccccccgagtggtggtctctggaacctctgagcatggtggacctccc 742
|||||
Db 61 TGCCCCCAGAGCCCCCAGATGTGGTGTCTCTGACCCCTGAGCATGTGAGCGCTTAC 120
|||||
QY 743 agggccgagccccagctacgttctctga-----agccagaggtgttactatga 793
|||||

```

```

Db 121 AGGCCGGAAGCCCGCCAGCTATCGCTCTGATTTTCTGATTTTCTGATTTTCTGTTT 180
QY 794 catctctcttattattattattattattattattattattattattattattattatt 847
|||||
Db 181 GGTTCCTCCACTTATTATTACGGGTATTATTATTATTATTATTATTATTATTATTCTT 240
|||||
QY 848 acttgagataataagaggttccagagaggat 879
|||||
Db 241 ACTTGGAATATATAAGAGCTTTGAAGAAAAAT 272
|||||

RESULT 8
BG389761 866 bp mRNA EST 12-MAR-2001
LOCUS BG389761 NIH_MGC_92 Homo sapiens cDNA clone IMAGE:4523457 5',
DEFINITION mRNA sequence.
ACCESSION BG389761.1 GI:13283197
VERSION BG389761 EST.
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 866)
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
CDNA distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10426 row: C column: 10
High quality sequence stop: 573.
FEATURES
source
Location/Qualifiers
1..866
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4523457"
/clone_lib="NIH_MGC_92"
/tissue_type="embryonal carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/notes="Organ: testis; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally; oligo-gt primed.
Average insert size 2.5 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
BASE COUNT 350 a 141 c 223 g 152 t
ORIGIN
Query Match 9.7%; Score 115.6; DB 153; Length 866;
Best Local Similarity 89.9%; Pred. No. 1.4e-10;
Matches 124; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 1053 tgcactccagcccgccagcagcgagattccatctcaaaaaataataataa 1112
|||||
Db 417 TGCACCTCAGCTGGCAACAGAGAGCTCCATCTCAAAAAAAAAAAAAAAAAAAAA 476
|||||
QY 1113 ataataataataataataataataataataataataataataataa 1172
|||||
Db 477 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 536
|||||
QY 1173 aaaaaaaaaaaaaaaaaaa 1190
|||||
Db 537 AAAAAAAAAAAAAAAAAAAAA 554
|||||

RESULT 9

```



```

RESULT 4
US-09-073-569-1
; Sequence 1, Application US/09073569
; Patent No. 6084088
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Grossmann, Angelika
; TITLE OF INVENTION: NOVEL TUMOR ANTIGENS
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZymoGenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/073,569
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Sawislak, Deborah A
; REGISTRATION NUMBER: 37,438
; REFERENCE/DOCKET NUMBER: 97-14
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6672
; TELEFAX: 206-442-6678
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1733 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single

```

Query Match 7.4%; Score 88; DB 1; Length 6671;
Best Local Similarity 90.4%; Pred. No. 1.8e-08;
Matches 94; Conservative 0; Mismatches 10; Indels

Dy	1086	atctcaaaaaataaataaaataaaaataataataaaaaaa	1145
Db	6568	ATCTGAAAAAATAAAAAAAAAAAAAAAAAAAAAAAAAAA	6627

```

TITLE OF INVENTION: Thereof
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: Howson and Howson
STREET: Spring House Corporate Cntr, P.O. Box 457
CITY: Spring House
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19477
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/02275
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/280,443
FILING DATE: 25-JUL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/197,794
FILING DATE: 17-FEB-1994
ATTORNEY/AGENT INFORMATION:
NAME: Bak, Mary E.
REGISTRATION NUMBER: 31,215
REFERENCE/DOCKET NUMBER: WST49BPCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-540-9206
TELEFAX: 215-540-5818
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 6671 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
MOLECULE TYPE: cdna
FEATURE:
NAME/KEY: CDS
LOCATION: 155..3832
PCT-US95-02275-1

Query Match          7.4%; Score 88; DB 5; Length 6671;
Best Local Similarity 90.4%; Pred.No. 1.8e-08;
Matches      94; Conservative    0; Mismatches   10; Indels     0; Gaps

QY   1086 atctcaaaaaataaatatgaataaaatgaaaataatataatataaaataaaaaaaaaaaaaa 1145
       ||||| |||||| | || | || | || | || | || | || | || | || | || | || |
Db    6568 ATCTGAAAAAATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 6627
       ||||| |||||| | || | || | || | || | || | || | || | || | || | || |

QY   1146 aaaaaaiaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaa 1189
       ||||| |||||| | || | || | || | || | || | || | || | || | || | || |
Db    6628 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 6671
       ||||| |||||| | || | || | || | || | || | || | || | || | || | || |

RESULT           9
US-08-628-417-5
Sequence 5, Application US/08628417
Patent No. 5627054
GENERAL INFORMATION:
APPLICANT: GILLESPIE, DAVID
TITLE OF INVENTION: COMPETITOR PRIMER ASYMMETRIC
POLYMERASE CHAIN REACTION
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSER: U.S. ARMY CHEMICAL AND BIOLOGICAL
DEFENSE COMMAND
STREET: OFFICE OF THE CHIEF COUNSEL (AMSCB-GC)
CITY: ABERDEEN PROVING GROUND
STATE: MARYLAND
COUNTRY: USA

```


Query Match 7.3%; Score 87.2; DB 1; Length 240;
Best Local Similarity 84.5%; Pred. No. 1.2e-08;
Matches 98; Conservative 0; Mismatches 18; Indels

Oy	1075	agcgagattccatctcagaataaaataaaataaaataaaataaaaaa	1134
D6	25	AGAAATATTTTTACTAAAAAATAAAAAAAAAAAAAAAAAAAAAA	84

[illegible]

RESULT 11

US-09-247-373B-33
; Sequence 33, Application US/09247373B
; Patent No. 6168954

```

: GENERAL INFORMATION:
: APPLICANT: MCGONIGLE, BRIAN
: APPLICANT: O'KEEFE, DANIEL
: TITLE OF INVENTION: SOYBEAN GLUTATHIONE-S-TRANSFERASE ENZYMES
: FILE REFERENCE: CL-1108-A
: CURRENT APPLICATION NUMBER: US/09/247,373B
: CURRENT FILING DATE: 1999-02-10
: PRIOR APPLICATION NUMBER: 08/924,747
: PRIOR FILING DATE: 1997-09-05
:

```

```

; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: Microsoft Office 97

```

```

; SEQ ID NO 33
; LENGTH: 1117

```

```

;
; LENGTH: 1117
;
; TYPE: DNA
;
; ORGANISM: SOYBEAN
;
; FEATURE:

```

```

; NAME/KEY: unsure
; LOCATION: (1101)
; OTHER INFORMATION: M=A OR C

```

```

; NAME/KEY: unsure
; LOCATION: (1104)
; OTHER INFORMATION: M=A OR C

```

; NAME/KEY: unsure
; LOCATION: (1116)

OTHER INFORMATION: N=G or A or T or C
US-09-247-373B-33

Query Match 7.3%; Score 87.2; DB 4; Length 1117;
Best Local Similarity 81.5%; Pred. No. 1.7e-08;
Matches 101; Conservative 0; Mismatches 23; Indels 0

QY 1067 ggcacagaggcagattccatctcaaaaaataaaataaaaataaatataa 1126
||| | | ||| | | ||| | | ||| | | ||| | | ||| | | ||| | |
Db 971 ggcaataaatcatgaattcaattctttaaaaaaaaaaaaaaaaaaaaaa 1030
||||| | | ||| | | ||| | | ||| | | ||| | | ||| | | ||| | |

[illegible]

Ddb	I031	aaaaaaaaaaaaaaaaaaaaaaaaaaaaaa	1090
Oy	I187	aaa	1190


```
Db 1091 aaca 1094
RESULT 12
US-08-821-994-64
; Sequence 64, Application US/08821994A
; Patent No. 6228643
; GENERAL INFORMATION:
; APPLICANT: Greenland, Andrew J
; APPLICANT: Thomas, Didier RP
; APPLICANT: Jepson, Ian
; TITLE OF INVENTION: Promoters
; FILE REFERENCE: PPD 50108
; CURRENT APPLICATION NUMBER: US/08/821,994A
; CURRENT FILING DATE: 1997-03-22
; EARLIER APPLICATION NUMBER: PCT/GB97/00729
; EARLIER FILING DATE: 1997-03-18
; EARLIER APPLICATION NUMBER: GB 9606062.9
; EARLIER FILING DATE: 1996-03-22
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 64
; LENGTH: 1474
; TYPE: DNA
; ORGANISM: Brassica napus
US-08-821-994-64

Query Match 7.3%; Score 87; DB 4; Length 1474;
Best Local Similarity 90.3%; Pred. No. 2e-08;
Matches 93; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 1087 tctcaaaaaataaataaataaataaataaataaataaataaataaataaataa 1146
Db 1372 tctcaaaaaataaataaataaataaataaataaataaataaataaataa 1431

QY 1147 aaaaaataaataaataaataaataaataaataaataaataaataa 1189
Db 1432 aaaaaataaataaataaataaataaataaataaataaataaataa 1474

RESULT 13
US-08-702-344-26
; Sequence 26, Application US/08702344
; Patent No. 5723315
; GENERAL INFORMATION:
; APPLICANT: Jacobs, Kenneth
; APPLICANT: McCoy, John
; APPLICANT: LaVallie, Edward
; APPLICANT: Racie, Lisa
; APPLICANT: Treacy, Maurice
; APPLICANT: Spaulding, Vikki
; TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE:
; APPLICATION NUMBER: US/08/702,344
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Sprunger, Suzanne A.
; REGISTRATION NUMBER: 41,323
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8284
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2447 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA

NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8224
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 144 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-702-344-26

Query Match 7.3%; Score 86.4; DB 1; Length 144;
Best Local Similarity 89.4%; Pred. No. 1.5e-08;
Matches 93; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 1087 tctcaaaaaataaataaataaataaataaataaataaataaataaataa 1146
Db 19 TTTTAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 78

QY 1147 aaaaaataaataaataaataaataaataaataaataaataaataa 1190
Db 79 AAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 122

RESULT 14
US-09-014-969-14
; Sequence 14, Application US/09014969
; Patent No. 5965397
; GENERAL INFORMATION:
; APPLICANT: Jacobs, Kenneth
; APPLICANT: McCoy, John M.
; APPLICANT: LaVallie, Edward R.
; APPLICANT: Racie, Lisa A.
; APPLICANT: Merberg, David
; APPLICANT: Treacy, Maurice
; APPLICANT: Spaulding, Vikki
; APPLICANT: Agostino, Michael J.
; TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: MA
; COUNTRY: U.S.A.
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE:
; APPLICATION NUMBER: US/09/014,969
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Sprunger, Suzanne A.
; REGISTRATION NUMBER: 41,323
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8284
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2447 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
```


GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 6, 2001, 21:09:14 ; Search time 163 Seconds
(without alignments)
4584.067 Million cell updates/sec

Title: US-09-391-861-1

Perfect score: 1190

Sequence: 1 gagatccagccgaagagg.....aaaaaaaaaaaaaaaaaaaaa 1190

Scoring table:

IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 730101 seqs, 313950809 residues

Total number of hits satisfying chosen parameters: 1460202

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_0601.*

1:	/SID88/gcgdata/geneseq/geneseq/NA1980.DAT.*
2:	/SID88/gcgdata/geneseq/geneseq/NA1981.DAT.*
3:	/SID88/gcgdata/geneseq/geneseq/NA1982.DAT.*
4:	/SID88/gcgdata/geneseq/geneseq/NA1983.DAT.*
5:	/SID88/gcgdata/geneseq/geneseq/NA1984.DAT.*
6:	/SID88/gcgdata/geneseq/geneseq/NA1985.DAT.*
7:	/SID88/gcgdata/geneseq/geneseq/NA1986.DAT.*
8:	/SID88/gcgdata/geneseq/geneseq/NA1987.DAT.*
9:	/SID88/gcgdata/geneseq/geneseq/NA1988.DAT.*
10:	/SID88/gcgdata/geneseq/geneseq/NA1989.DAT.*
11:	/SID88/gcgdata/geneseq/geneseq/NA1990.DAT.*
12:	/SID88/gcgdata/geneseq/geneseq/NA1991.DAT.*
13:	/SID88/gcgdata/geneseq/geneseq/NA1992.DAT.*
14:	/SID88/gcgdata/geneseq/geneseq/NA1993.DAT.*
15:	/SID88/gcgdata/geneseq/geneseq/NA1994.DAT.*
16:	/SID88/gcgdata/geneseq/geneseq/NA1995.DAT.*
17:	/SID88/gcgdata/geneseq/geneseq/NA1996.DAT.*
18:	/SID88/gcgdata/geneseq/geneseq/NA1997.DAT.*
19:	/SID88/gcgdata/geneseq/geneseq/NA1998.DAT.*
20:	/SID88/gcgdata/geneseq/geneseq/NA1999.DAT.*
21:	/SID88/gcgdata/geneseq/geneseq/NA2000.DAT.*
22:	/SID88/gcgdata/geneseq/geneseq/NA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	495	41.6	514	22	AAF76715
2	401.8	33.8	659	21	AAAF75631
3	107.4	9.0	1457	21	AAAG1287
4	95.2	8.0	1376	20	AAAX04325
5	94.8	8.0	876	21	AAAS9201
6	94.6	7.9	3213	20	AAV55742
7	94	7.9	667	21	AAAC59098
8	92.8	7.8	1722	21	AAAC71124
9	92.4	7.8	1529	21	AAAC59838
10	92.2	7.7	2082	19	AAV41257
11	91.8	7.7	1985	21	AAAC59406

12	91.6	7.7	936	20	AAZ06226	Human secreted pro
13	91.6	7.7	2753	22	AA991862	Human secreted pro
14	91.4	7.7	396	22	AAF94862	Human ovarian can
15	91	7.6	1259	13	AAQ23028	Clone W264 encodin
16	91	7.6	1388	21	AAQ59295	Human secreted pro
17	90.8	7.6	550	19	AAV41916	Nucleotide sequenc
18	90.8	7.6	905	21	AAAG4642	Partial sequence M
19	90.4	7.6	1733	21	AAA37036	Human PRO1411 (UNQ
20	90.4	7.6	1733	22	AA954238	DNA encoding prote
21	90.4	7.6	1734	22	AAF92083	Human PRO1411 cDNA
22	90.4	7.6	1734	22	AAAC87038	Nucleotide sequenc
23	89.8	7.5	3508	21	AAA16619	Human secreted pro
24	89.8	7.5	4909	22	AAF24165	Human secreted pro
25	89.6	7.5	882	21	AAZ52528	Human secreted pro
26	89.6	7.5	909	21	AACT9961	Human secreted pro
27	89.6	7.5	1690	21	AAZ90632	Human adipose tiss
28	89.6	7.5	2186	22	AAF73412	Grand fir monoterp
29	89.4	7.5	876	21	AAAC63439	Human fetal brain
30	89.4	7.5	1936	21	AAZ43798	Human gene express
31	89.2	7.5	300	20	AAZ14372	Coding sequence fo
32	89.2	7.5	772	19	AAV58363	Partial sequence M
33	89.2	7.5	801	21	AAAG4638	Human ZALPHA29 DNA
34	89.2	7.5	813	22	AAF31470	Human secreted pro
35	89.2	7.5	959	21	AAZ26370	Human secreted pro
36	89.2	7.5	1149	21	AAAC81030	CDNA from clone cr
37	89.2	7.5	2496	19	AAV63189	Norwalk virus stra
38	89.2	7.5	7753	15	AAQ56826	Human ovarian can
39	89	7.5	396	22	AAF94842	pl35-NT3 construct
40	89	7.5	441	20	AAZ09474	Rat clone 70129147
41	89	7.5	872	22	AAF31060	Corn CCR4 transcri
42	89	7.5	1495	21	AAA27985	Human secreted pro
43	89	7.5	1751	21	AAAC68122	Human RNA helicase
44	89	7.5	4120	20	AAZ09473	Membrane-bound pro
45	88.8	7.5	2846	21	AAZ65034	

ALIGNMENTS

RESULT 1

AAF76715
ID AAF76715 standard; DNA; 514 BP.

XX AAF76715;

XX 17-MAY-2001 (first entry)

DE Human fibroblast growth factor 19 homologue FGF19X coding sequence.

XX Human; fibroblast growth factor 19; FGF19X; embryonic development;

KW proliferative disorder; cancer; restenosis; psoriasis;

KW rheumatoid arthritis; Dupuytren's contracture; ds.

XX Homo sapiens.

OS Homo sapiens.

XX WO200118209-A1.

XX 15-MAR-2001.

XX 08-SEP-2000; 2000WO-US24863.

XX 10-SEP-1999; 99US-0153303.

PR 03-APR-2000; 2000US-0194246.

PR 19-JUL-2000; 2000US-0619251.

XX (CURA-) CURAGEN CORP.

XX Shimkets RA, Vernet C, Burgess C, Fernandes E, Taupier R;

PI Quinn KE, Spyteck KA, Rastelli L, Herrmann JL;

XX WPI; 2001-218559/22.

DR P-PSDB; AAB/3069.

XX

PT Fibroblast growth factor-19x polypeptides and polynucleotides useful
PT for diagnosis, prevention, treatment of proliferative, differentiative,
PT tumorigenic disorders such as tumor, psoriasis, rheumatoid arthritis -
XX
XX Claim 3; Page 7; 97pp; English.

XX The present invention describes the protein and coding sequences of the
XX human fibroblast growth factor (FGF) 19 homologue FGF19X, the latter of
XX which is shown here. The sequences can be used in the prognosis and
XX treatment of proliferative diseases such as cancer, restenosis,
XX psoriasis, rheumatoid arthritis and Dupuytren's contracture, as well as
XX to stimulate cell growth for treating neurological disorders such as
XX Alzheimer's disease.

XX Sequence 514 BP; 103 A; 157 C; 155 G; 99 T; 0 other;

Query Match 41.6%; Score 495; DB 22; Length 514;
Best Local Similarity 100.0%; Pred. No. 3e-64;
Matches 495; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 91 cagcttcctcagctcaccaccccgagatcacctgagaccgagccattgatgactcg 150
DB 1 cagcttcctcagctcaccaccccgagatcacctgagaccgagccattgatgactcg 60
QY 151 gacgagaccgggttcgagacactcagactgtgggtttctgtgctggtcttcctgctg 210
DB 61 gacgagaccgggttcgagacactcagactgtgggtttctgtgctggtcttcctgctg 120
QY 211 ggaagctgcagggcacacccaccctcactgactcagctcctcctcaattcggggccaa 270
DB 121 ggaagctgcagggcacacccaccctcactgactcagctcctcctcaattcggggccaa 180
QY 271 gtcggcagcgttacctctacacagatgatcccgagcagacagccacactggagatc 330
DB 181 gtcggcagcgttacctctacacagatgatcccgagcagacagccacactggagatc 240
QY 331 aaggagatggagcaggtggggcgctgctgaccagaccccgaaagtctcctcagctg 390
DB 241 aaggagatggagcaggtggggcgctgctgaccagaccccgaaagtctcctcagctg 300
QY 391 aaagccttgaagccgggaggtattcaaatcttgggagtcacagacatccaggctcctgtgc 450
DB 301 aaagccttgaagccgggaggtattcaaatcttgggagtcacagacatccaggctcctgtgc 360
QY 451 cagcgccagatggggccctgtatgatcgtccactttgacctgagccctgcagcttc 510
DB 361 cagcgccagatggggccctgtatgatcgtccactttgacctgagccctgcagcttc 420
QY 511 cgggagctcttcttgagacgagatacaatgtttaccagtcgacgacgacgctcccg 570
DB 421 cgggagctcttcttgagacgagatacaatgtttaccagtcgacgacgacgctcccg 480
QY 571 ctgacactgccaggg 585
DB 481 ctgacactgccaggg 495

RESULT 2

AAA75631
ID AAA75631 standard; DNA; 659 BP.
XX
XX AAA75631;
XX
XX 22-JAN-2001 (first entry)
XX
XX Nucleotide sequence of murine fibroblast growth factor (FGF)-21.

XX pd10-VEGFuc; gene delivery vector; eye disease; neovascular disease;
KW neurotrophic factor; anti-angiogenic factor; eye disease; glaucoma;
KW macular degeneration; diabetic retinopathy; retinitis pigmentosa;
KW inherited retinal degeneration; surgery-induced retinopathy;
KW retinal detachment; photic retinopathy; toxic retinopathy;

KW trauma-induced retinopathy; wet age related macular degeneration;
KW ARMD; retinopathy; fibroblast growth factor-20; FGF-20; ss.

XX Mus sp.

XX Key Location/Qualifiers
XX CDS 14..646
XX FT /*tag= a
XX FT /product= "Fibroblast growth factor 21"

XX W0200054813-A2.

XX 21-SEP-2000.

XX 15-MAR-2000; 2000WO-US07062.

XX 15-MAR-1999; 99US-0124460.

XX 06-JAN-2000; 2000US-0174984.

XX (CHIR) CHIRON CORP.

XX (REGC) UNIV CALIFORNIA.

XX Manning WC, Dwarki VJ, Rendahl K, Zhou S, McGee LH, Lau D;
XX Flannery JG, Miller S, Wang F, Di Polo A;

XX WPI; 2000-618862/59.

XX P-PSDB; AAB18636.

XX Treating or preventing eye diseases or inhibiting neovascular disease
XX of the eye, comprises intraocularly administering a gene delivery
XX vector that directs expression of neurotrophic factors or
XX anti-angiogenic factors -
XX Disclosure; Fig 30; 86pp; English.

XX The present sequence encodes a murine fibroblast growth factor (FGF)
XX -21. FGF-20 is expressed using a gene delivery vector of the invention.
XX Vectors of the invention are used for treating or preventing eye
XX diseases, or inhibiting neovascular disease of the eye. The gene
XX delivery vector directs the expression of one or more neurotrophic
XX factors, or anti-angiogenic factors, such that the disease of the eye
XX is prevented or treated. The gene delivery vectors are useful for
XX treating or preventing diseases of the eye such as macular degeneration,
XX diabetic retinopathy, inherited retinal degeneration such as retinitis
XX pigmentosa, glaucoma, surgery-induced retinopathy, retinal detachment,
XX photic retinopathy, toxic retinopathy or trauma-induced retinopathy and
XX for inhibiting neovascular diseases such as wet age related macular
XX degeneration (ARMD) or retinopathy of prematurity.

XX Sequence 659 BP; 140 A; 208 C; 179 G; 132 T; 0 other;

Query Match 33.8%; Score 401.8; DB 21; Length 659;
Best Local Similarity 80.7%; Pred. No. 1.1e-50;
Matches 469; Conservative 0; Mismatches 112; Indels 0; Gaps 0;

QY 191 tgcctggctggtctctctgctggagcctccagggcacaccccatccctgactccagctc 250
DB 66 tgcctggctggtctctctgctggagcctccagggcacaccccatccctgactccagc 125
QY 251 tctctgcaattcgggggccaaagtcgagcgggtacctctacacagatgatgccacagaga 310
DB 126 tcctccagatttgggggtcaagtcgagcgggtacctctacacagatgatgccacagaga 195
QY 311 cagaagccaccctgagatcaggagatgggacggtggggcgctgctgacacagagcc 370
DB 186 ctgaagccaccctgagatcaggagatgggacggtggggcgctgctgacacagagcc 245
QY 371 ccgaaagtctctcctcagctgaaagccttgaagccgggaggtatttcaaatcttgggagtc 430
DB 246 cagaagtcctcctgagctcaaaagccttgaagccaggggtcattcaaatcttgggtgca 305
QY 431 agacatccaggttctcctgtgcagcgccagatggggccctgtatggtatcgtccacttg 490

CC	and include products for the diagnosis or treatment of cancer, tumours,
CC	AIDS, autoimmune disorders, allergy, cardiovascular disorders, viral,
CC	bacterial and fungal infection. The genes are used to generate fusion
CC	proteins by linking to the gene a human immunoglobulin portion (AAA61251)
CC	for increasing stability of the fused protein as compared to the
CC	secreted protein only.
XX	
SQ	Sequence 1457 BP; 440 A; 340 C; 307 G; 370 T; 0 other;
Query Match	9.0%; Score 107.4; DB 21; Length 1457;
Best Local Similarity	80.3%; Pred. No. 7.6e-08;
Matches 126; Conservative	0; Mismatches 31; Indels 0; Gaps
Qy 1034	ttgagcggagtcgtctgtcactccagccagcgccacagagcgagatccatctcaaa 1093
Db	
1276	tttagtcttgtgtgcactgcagccgctgggcaacaagagcgaaactctgtcaaa 1335
Qy 1094	aaataaataataataataataataataataataataataataataataataataa 1153
Db	
1336	aaaaaataaaaaaataaaaaaataaaaaaataaaaaaataaaaaaataaaaaa 1395
Qy 1154	aaaaaataaaaaaataaaaaaataaaaaaataaaaaaataaaaaaataaaaaa 1190
Db	
1396	aaaaaataaaaaaataaaaaaataaaaaaataaaaaaataaaaaaataaaaaa 1432
RESULT 4	
AAAX04325	
ID	AXX04325 standard; DNA; 1376 BP.
XX	
AC	AAAX04325;
XX	
DT	13-APR-1999 (first entry)
XX	
DE	Human secreted protein gene 15 clone HSDES04.
XX	
KW	Human; secreted protein; fusion protein; gene therapy; protein therapy;
KW	diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia
KW	developmental abnormality; foetal deficiency; blood; allergy; renal; ds;
KW	immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;
KW	inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;
KW	cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus
KW	osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;
KW	endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
OS	Homo sapiens.
XX	
FN	W09856804-A1.
XX	
PD	17-DEC-1998.
XX	
PF	11-JUN-1998; 98WO-US12125.
XX	
PR	02-OCT-1997; 97US-0061060.
PR	13-JUN-1997; 97US-0049547.
PR	13-JUN-1997; 97US-0049548.
PR	13-JUN-1997; 97US-0049549.
PR	13-JUN-1997; 97US-0049550.
PR	13-JUN-1997; 97US-0049606.
PR	13-JUN-1997; 97US-0049607.
PR	13-JUN-1997; 97US-0049608.
PR	13-JUN-1997; 97US-0049609.
PR	13-JUN-1997; 97US-0049610.
PR	13-JUN-1997; 97US-0049611.
PR	13-JUN-1997; 97US-0050366.
PR	13-JUN-1997; 97US-0050367.
PR	13-JUN-1997; 97US-0050368.
PR	13-JUN-1997; 97US-0050369.
PR	13-JUN-1997; 97US-0050370.
PR	13-JUN-1997; 97US-0050371.
PR	13-JUN-1997; 97US-0050372.
PR	13-JUN-1997; 97US-0050373.
PR	13-JUN-1997; 97US-0050374.
PR	13-JUN-1997; 97US-0050375.
PR	13-JUN-1997; 97US-0050376.
PR	13-JUN-1997; 97US-0050377.
PR	13-JUN-1997; 97US-0050378.
PR	13-JUN-1997; 97US-0050379.
PR	13-JUN-1997; 97US-0050380.
PR	13-JUN-1997; 97US-0050381.
PR	13-JUN-1997; 97US-0050382.
PR	13-JUN-1997; 97US-0050383.
PR	13-JUN-1997; 97US-0050384.
PR	13-JUN-1997; 97US-0050385.
PR	13-JUN-1997; 97US-0050386.
PR	13-JUN-1997; 97US-0050387.
PR	13-JUN-1997; 97US-0050388.
PR	13-JUN-1997; 97US-0050389.
PR	13-JUN-1997; 97US-0050390.
PR	13-JUN-1997; 97US-0050391.
PR	13-JUN-1997; 97US-0050392.
PR	13-JUN-1997; 97US-0050393.
PR	13-JUN-1997; 97US-0050394.
PR	13-JUN-1997; 97US-0050395.
PR	13-JUN-1997; 97US-0050396.
PR	13-JUN-1997; 97US-0050397.
PR	13-JUN-1997; 97US-0050398.
PR	13-JUN-1997; 97US-0050399.
PR	13-JUN-1997; 97US-0050400.
PR	13-JUN-1997; 97US-0050401.
PR	13-JUN-1997; 97US-0050402.
PR	13-JUN-1997; 97US-0050403.
PR	13-JUN-1997; 97US-0050404.
PR	13-JUN-1997; 97US-0050405.
PR	13-JUN-1997; 97US-0050406.
PR	13-JUN-1997; 97US-0050407.
PR	13-JUN-1997; 97US-0050408.
PR	13-JUN-1997; 97US-0050409.
PR	13-JUN-1997; 97US-0050410.
PR	13-JUN-1997; 97US-0050411.
PR	13-JUN-1997; 97US-0050412.
PR	13-JUN-1997; 97US-0050413.
PR	13-JUN-1997; 97US-0050414.
PR	13-JUN-1997; 97US-0050415.
PR	13-JUN-1997; 97US-0050416.
PR	13-JUN-1997; 97US-0050417.
PR	13-JUN-1997; 97US-0050418.
PR	13-JUN-1997; 97US-0050419.</

PT-² Novel nucleic acids and peptides derived from open reading frame X,

PR 17-MAR-1999; 99US-0124808.

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 6, 2001, 21:05:44 ; Search time 2566.06 Seconds
(without alignments)
7173.106 Million cell updates/sec

Title: US-09-391-861-1
Perfect score: 1190
Sequence: 1 gaggatccagccgaagagg.....aaaaaaaaaaaaaaaaaaaa 1190

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1344157 seqs, 7733874588 residues 2688314
Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl:*
1: gb_ba1:*
2: gb_ba2:*
3: gb_ba3:*
4: gb_in1:*
5: gb_in2:*
6: gb_in3:*
7: gb_om:*
8: gb_ov:*
9: gb_pat1:*
10: gb_pat2:*
11: gb_ph:*
12: gb_pl1:*
13: gb_pl2:*
14: gb_pl3:*
15: gb_pl4:*
16: em_ba1:*
17: em_ba2:*
18: em_fun:*
19: em_htgo_hum:*
20: em_htgo_inv:*
21: em_htgo_rod:*
22: em_htg_hum1:*
23: em_htg_hum2:*
24: em_htg_hum3:*
25: em_htg_hum4:*
26: em_htg_hum5:*
27: em_htg_hum6:*
28: em_htg_hum7:*
29: em_htg_hum8:*
30: em_htg_inv1:*
31: em_htg_inv2:*
32: em_htg_other:*
33: em_htg_rod:*
34: em_hum1:*
35: em_hum2:*
36: em_hum3:*
37: em_hum4:*
38: em_hum5:*
39: em_hum6:*
40: em_hum7:*
41: em_in:*
42: em_om:*
43: em_or:*

44: em_ov:*
45: em_pat:*
46: em_ph:*
47: em_pl:*
48: em_ro:*
49: em_sts:*
50: em_sy:*
51: em_un:*
52: em_v1:*
53: gb_sts1:*
54: gb_sts2:*
55: gb_sts3:*
56: gb_sy:*
57: gb_un:*
58: gb_v11:*
59: gb_v12:*
60: gb_htg1:*
61: gb_htg2:*
62: gb_htg3:*
63: gb_htg4:*
64: gb_htg5:*
65: gb_htg6:*
66: gb_htg7:*
67: gb_htg8:*
68: gb_htg9:*
69: gb_htg10:*
70: gb_htg11:*
71: gb_htg12:*
72: gb_htg13:*
73: gb_htg14:*
74: gb_htg15:*
75: gb_htg16:*
76: gb_htg17:*
77: gb_htg18:*
78: gb_htg19:*
79: gb_htg20:*
80: gb_htg21:*
81: gb_htg22:*
82: gb_htg23:*
83: gb_htg24:*
84: gb_htg25:*
85: gb_pri:*
86: gb_pr2:*
87: gb_pr3:*
88: gb_pr4:*
89: gb_pr5:*
90: gb_pr6:*
91: gb_pr7:*
92: gb_pr8:*
93: gb_pr9:*
94: gb_rol:*
95: gb_rod2:*
96: gb_in4:*
97: gb_pri0:*
98: em_ba3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	628.4	52.8	630	85	AB021975 Homo sapi
2	575	48.3	37402	87	AC009002 Homo sapi
3	563	47.3	110000	60	AC008749 Homo sapi
4	563	47.3	110000	60	Continuation (2 of
5	556.2	46.7	4033	85	AB006136 Homo sapi
6	495	41.6	514	10	AX097639 Sequence
7	435.8	36.6	227949	70	AC026803 Homo sapi
8	412.6	34.7	179538	68	AC024740 Homo sapi

ALIGNMENTS

```

RESULT 1
LOCUS AB0211975 630 bp mRNA PRI 03-AUG-2000
DEFINITION Homo sapiens mRNA for FGF-21, complete cds.
ACCESSION AB021975
VERSION AB021975.1 GI:9049444
KEYWORDS new FGF.
SOURCE Homo sapiens cDNA to mRNA.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (sites)
AUTHORS Nishimura,T., Nakatake,Y., Konishi,M. and Itoh,N.
TITLE Identification of a novel FGF, FGF-21, preferentially expressed in
the liver(1)
MEDLINE 20461777
REFERENCE 2 (bases 1 to 630)
AUTHORS Itoh,N.
TITLE Direct Submission
JOURNAL Submitted (29-DEC-1998) to the DDBJ/EMBL/GenBank databases.
Nobuyuki Itoh, Kyoto University, Graduate School of Pharmaceutical
Sciences, Department of Genetic Biochemistry; Yoshida-Shimoadachi,
Sakyo, Kyoto, Kyoto 606-8501, Japan
(E-mail: itohnobu@pharm.kyoto-u.ac.jp. Tel:81-75-753-4540,
Fax:81-75-753-4600)
COMMENT Sequence updated (17-Mar-1999).
FEATURES             Location/Qualifiers
     source            1..630
                        /organism="Homo sapiens"
                        /db_xref="taxon:9606"

```


6233	7544:	contig	of 1312	bp in length
7545	7644:	gap	of unknown	length
7645	8892:	contig	of 1248	bp in length
8893	10296:	gap	of unknown	length
8993	10296:	contig	of 1304	bp in length
10297	10396:	gap	of unknown	length
10397	11725:	contig	of 1329	bp in length
11726	11825:	gap	of unknown	length
11826	13734:	contig	of 1909	bp in length
13735	13834:	gap	of unknown	length
13835	15036:	contig	of 1222	bp in length
15057	15156:	gap	of unknown	length
15157	16358:	contig	of 1202	bp in length
16359	16458:	gap	of unknown	length
16459	17875:	contig	of 1417	bp in length
17876	17975:	gap	of unknown	length
17976	19527:	contig	of 1552	bp in length
19528	19627:	gap	of unknown	length
19628	21424:	contig	of 1797	bp in length
21425	21524:	gap	of unknown	length
21525	22793:	contig	of 1369	bp in length
22794	22893:	gap	of unknown	length
22894	23905:	contig	of 1012	bp in length
23906	24003:	gap	of unknown	length
24006	25440:	contig	of 1435	bp in length
25441	25540:	gap	of unknown	length
25541	26895:	contig	of 1355	bp in length
26896	26995:	gap	of unknown	length
26996	28178:	contig	of 1183	bp in length
28179	28278:	gap	of unknown	length
28279	29887:	contig	of 1609	bp in length
29888	29987:	gap	of unknown	length
29988	31869:	contig	of 1882	bp in length
31870	31969:	gap	of unknown	length
31970	33535:	contig	of 1566	bp in length
33536	33635:	gap	of unknown	length
33636	34963:	contig	of 1328	bp in length
34964	35063:	gap	of unknown	length
35064	36881:	contig	of 1818	bp in length
36882	36981:	gap	of unknown	length
36982	38148:	contig	of 1167	bp in length
38149	38248:	gap	of unknown	length
38249	39889:	contig	of 1641	bp in length
39890	39989:	gap	of unknown	length
39990	41963:	contig	of 1974	bp in length
41964	42063:	gap	of unknown	length
42064	43733:	contig	of 1670	bp in length
43734	43833:	gap	of unknown	length
43834	45414:	contig	of 1581	bp in length
45415	45514:	gap	of unknown	length
45515	47046:	contig	of 1532	bp in length
47047	47146:	gap	of unknown	length
47147	48965:	contig	of 1819	bp in length
48966	49065:	gap	of unknown	length
49066	51369:	contig	of 2304	bp in length
51370	51469:	gap	of unknown	length
51470	53128:	contig	of 1659	bp in length
53129	53228:	gap	of unknown	length
53229	54480:	contig	of 1252	bp in length
54481	54580:	gap	of unknown	length
54581	56485:	contig	of 1905	bp in length
56486	56585:	gap	of unknown	length
56586	58664:	contig	of 2079	bp in length
58665	58764:	gap	of unknown	length
58765	59595:	contig	of 1195	bp in length
59596	60059:	gap	of unknown	length
60060	62303:	contig	of 2244	bp in length
62304	62403:	gap	of unknown	length
62404	64204:	contig	of 1801	bp in length
64205	64304:	gap	of unknown	length
64305	66196:	contig	of 1892	bp in length
66197	66296:	gap	of unknown	length
66297	67878:	contig	of 1582	bp in length

*	67879	67978:	gap of	unknown	length
*	69965:	contig of	1987	bp	in length
*	69366	70065:	gap of	unknown	length
*	70066	71633:	contig of	1568	bp in length
*	71634	71733:	gap of	unknown	length
*	71734	73978:	contig of	2245	bp in length
*	73979	74078:	gap of	unknown	length
*	74079	76073:	contig of	1995	bp in length
*	76074	76173:	gap of	unknown	length
*	76174	78463:	contig of	2296	bp in length
*	78470	78569:	gap of	unknown	length
*	78570	81250:	contig of	2681	bp in length
*	81251	81350:	gap of	unknown	length
*	81351	83762:	contig of	2412	bp in length
*	83763	83862:	gap of	unknown	length
*	83863	85089:	contig of	2127	bp in length
*	85990	86089:	gap of	unknown	length
*	86090	88156:	contig of	2067	bp in length
*	88157	88256:	gap of	unknown	length
*	88257	90318:	contig of	2062	bp in length
*	90319	90418:	gap of	unknown	length
*	90419	92289:	contig of	1871	bp in length
*	92290	92389:	gap of	unknown	length
*	92390	95174:	contig of	2785	bp in length
*	95175	95274:	gap of	unknown	length
*	95275	98333:	contig of	3059	bp in length
*	98334	98433:	gap of	unknown	length
*	98434	99775:	contig of	1542	bp in length
*	99776	100075:	gap of	unknown	length
*	100076	101499:	contig of	1424	bp in length
*	101500	101599:	gap of	unknown	length
*	101600	103848:	contig of	2249	bp in length
*	103849	103948:	gap of	unknown	length
*	103949	106127:	contig of	2179	bp in length
*	106128	106227:	gap of	unknown	length
*	106228	108402:	contig of	2175	bp in length
*	108403	108502:	gap of	unknown	length
*	108503	110948:	contig of	2446	bp in length
*	110949	111048:	gap of	unknown	length
*	111049	113905:	contig of	2857	bp in length
*	113906	114005:	gap of	unknown	length
*	114006	117256:	contig of	3251	bp in length
*	117257	117356:	gap of	unknown	length
*	117357	119135:	contig of	1779	bp in length
*	119136	119235:	gap of	unknown	length
*	119236	121325:	contig of	2090	bp in length
*	121326	121425:	gap of	unknown	length
*	121426	123954:	contig of	2529	bp in length
*	123955	124054:	gap of	unknown	length
*	124055	126951:	contig of	2797	bp in length
*	126952	126951:	gap of	unknown	length
*	126952	129652:	contig of	2701	bp in length
*	129653	129752:	gap of	unknown	length
*	129753	132233:	contig of	2481	bp in length
*	132234	132333:	gap of	unknown	length
*	132334	135268:	contig of	2935	bp in length
*	135269	135368:	gap of	unknown	length
*	135369	137746:	contig of	2378	bp in length
*	137747	137846:	gap of	unknown	length
*	137847	141549:	contig of	3703	bp in length
*	141550	141649:	gap of	unknown	length
*	141650	144391:	contig of	2742	bp in length
*	144392	144491:	gap of	unknown	length
*	144492	147414:	contig of	2923	bp in length

Query Match 47 3% Score 563 DB 60 Length 110000;

Best Local Similarity	97.3%	Pred. No. 1e-80;	Indels
Mismatches 592;	Conservative	0;	15;
Gaps		1;	1;

[illegible]

```
QY 538 aatgtttaccagtcgaagcccaaggcctcccgctgcacctgcccagggaaacaagtcccca 597
Db 109697 AATGTTTACCAAGTCCGAAGCCACAGGCTCCCGCTGCACCTGCCAGGGAACAAGTCCCCA 109638
QY 598 caccggaccctgcaccccgaggacagctcgcttccctgcactaccagggcctgcccccc 657
Db 109637 CACCGGACCCCTGCACCCCGAGGACCAAGCTGCGTTCCTGCGCATACACAGCCCTGCCCCC 109578
QY 658 gcaccccccaggacaccccggaatcctcgccccccagccccccgagtggtggcctcctcgac 717
Db 109577 GCACCCCGGAGCCACCCGGAATCCTGCGCCCCCAGCCCGCCGATGCGGCTCCTCGGAC 109518
QY 718 cctctgagcatggtggacctccagggccggaagccccagctacgtctcctgaaagccag 777
Db 109517 CCTCTGAGCATGCTGGGACCTTCCAGGCGCGAAGCCCGCCAGCTACGCTTCTCTGAAGCCAG 109458
QY 778 aggtgtttactatgacatcctcttattattattaggtattattattatttttttttttt 837
Db 109457 AGGCTGTTTACTATGACATCTCCTCTTTATTATTAGTTATTATTATTATTATTATT 109398
QY 838 tatttttcttacttgagataaagaagttccagagagagataagaatgagcatgtgtga 897
Db 109397 TATTTTCTTACTTGAGATAATAAGAGTTCCAGAGGAGGATAAGATGAGCATGTGTGA 109338
QY 898 gtgtcaggaagacaatgagcagctgtttgtctccctggccgggacaatccctctac 957
Db 109337 GTGTCTGAGGAAGACATGCGCAGCTGTTTGTCTCTGCGCCGACAAACCCCTCTAC 109278
QY 958 acctccctcacgtggtccgagagctggtgctccacacagggcctcacttttttttttt 1017
Db 109277 ACCTCCCTCACGTGTCGAGGCTGCTGGCTTCCACTGGGCTCACATTTTCTTTTTC 109218
QY 1018 ttttttttttttttttttttttttttttttttttttttttttttttttttttttttttt 1076
Db 109217 TTTTCTTTT-TTTTTTTTGAGACGAGTCTGCTCTGTGACCCAGCGTGGAGTGCAAGTG 109160

RESULT 4
AC008749_1/c
WPCOMMENT
Sequence split into 5 fragments LOCUS AC008749 Accession AC008749
Fragment Name Begin End
AC008749_0 1 110000
AC008749_1 100001 210000
AC008749_2 200001 310000
AC008749_3 300001 410000
AC008749_4 400001 467420
Continuation (2 of 5) of AC008749 from base 100001 (AC008749 Homo sapiens chromosome 19

Query Match 47.3%; Score 563; DB 60; Length 110000;
Best Local Similarity 97.3%; Pred. No. le-80;
Matches 583; Conservative 0; Mismatches 15; Indels 1; Gaps 1;

QY 478 tcgtctccacttgacactgagcctgcagcttcgagcttcgagctctcttgagacgatac 537
Db 9757 TAGCTCCACTTTGACCTCAGCGCTGCAGTTCGCGGAGCTGCTTCTTGAGGACGGATAC 9698
QY 538 aatgtttacagtcgaagcccaagcagcctcccgctgcactgccagggaaacaagtcccca 597
Db 9697 AATGTTTACAGTCCGAGAGCCCGGAGGACAGCTGCTGCTTCCCTGCCACTACCAAGCTGCCCCC 9638
QY 598 caccggaccctgcaccccgaggacagcagctcgcttccctgcactaccagggcctgcccccc 657
Db 9637 CACCGGACCCCTGCACCCCGAGGACCAAGCTGCTGCTTCCCTGCCACTACCAAGCTGCCCCC 9578
QY 658 gcaccccccaggacaccccggaatcctggccccccagcccccccgatggtggcctcctcgac 717
Db 9577 GCACCCCGGAGCCACCCGGAATCTGGCCCCCAGCCCGCCGATGCTGGCTCCTCGGAC 9518
QY 718 cctctgagcatggtggaccttccagggccggaagccccagctacgtctcctgaaagccag 777
Db 9517 CCTCTGAGCATGCTGGGACCTTCCAGGCGCGAAGCCCGCCAGCTACGCTTCTCTGAAGCCAG 9458
```

```
QY 778 aggtgtttactatgacatctcctcttattattattaggtattattattattattttttt 837
Db 9457 AGGCTGTTTACTATGACATCTCCTCTTTATTATTATTAGTTATTATTATTATTATT 9398
QY 838 tatttttcttacttgagataaagaagttccagagagataagaatgagcatgtgtga 897
Db 9397 TATTTTCTTACTTGAGATAATAAGAGTTCCAGAGGAGGATAAGATGAGCATGTGTGA 9338
QY 898 gtgtcaggggaagacatggcagcgtgtttgtctccctggccgggacaatccctctac 957
Db 9337 GTGTCTGAGGAAGACATGGCAGCTGTTTGTCTTCTTGGCCCGACAAACCCCTCTAC 9278
QY 958 acctccctcacgtggtccgagagctcctggcttccactcagggcctcacttttttttt 1017
Db 9277 ACCTCCCTCACGTGTCGAGGCTGCTGGCTTCCACTGGGCTCACATTTTCTTTTTC 9218
QY 1018 ttttttttttttttttttttttttttttttttttttttttttttttttttttttttttt 1076
Db 9217 TTTTCTTTT-TTTTTTTTGAGACGAGTCTGCTCTGTGACCCAGCGTGGAGTGCAAGTG 9160

RESULT 5
AB006136/c
LOCUS
DEFINITION Homo sapiens gene for alpha 1,2-fucosyltransferase, 5'flanking
region and partial cds.
ACCESSION AB006136
VERSION AB006136.1 GI:3242453
KEYWORDS FUT1; alpha (1, 2) fucosyltransferase.
SOURCE Homo sapiens peripheral leukocytes DNA.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (sites)
AUTHORS Koda,Y., Soejima,M. and Kimura,H.
TITLE Changing transcription start sites in H-type
alpha(1,2)fucosyltransferase gene (FUT1) during differentiation of
the human erythroid lineage
Eur. J. Biochem. 256 (2), 379-387 (1998)
98430978
2 (bases 1 to 4033)
Koda,Y.
Direct Submission
Submitted (04-AUG-1997) to the DDBJ/EMBL/GenBank databases. Yoshiro
Koda, Kurume University, School of Medicine, Department of Forensic
Medicine; Asahimachi 67, Kurume, Fukuoka 830-0011, Japan
(E-mail:ykoda@med.kurume-u.ac.jp. Tel:81-942-31-7554,
Fax:81-942-31-7700)
On Jun 20, 1998 this sequence version replaced gi:2317262.
COMMENT
Sequence updated (16-Jun-1998).
FEATURES
Location/Qualifiers
source
1..4033
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="19"
/map="19q13.3"
/tissue_type="peripheral leukocytes"
promoter
1..510
511..578
/gene="FUT1"
exon
/number=1
511..578
/gene="FUT1"
511..578
/gene="FUT1"
/standard_name="alpha(1,2)fucosyltransferase"
/codon_start=1
/product="FUT1"
/protein_id="BAA28952.1"
/db_xref="GI:3242453"
/translation="MGFHHVGQAGLELLTSGDLPAMV"
BASE COUNT 877 a 1242 c 1099 g 815 t
```



```
Center: Joint Genome Institute
Center Code: JGI
Web site: http://www.jgi.doe.gov
-----
Project Information
Center Project Name: 843459, BC808483
Center clone name: CITB-E1_263986
```

Summary Statistics

Consensus quality: 217198 bases at least Q40

Consensus quality: 224116 bases at least Q30

Consensus quality: 225875 bases at least Q20

Estimated insert size: 226670; agarose-fp estimation

Estimated insert size: 227399; sum-of-contigs estimation

Quality coverage: 6.85 in Q20 bases; agarose-fp estimation

Quality coverage: 6.83 in Q20 bases; sum-of-contigs estimation

* NOTE: This is a 'working draft' sequence. It currently

- * consists of 13 contigs. Gaps between the contigs
- * are represented as runs of N. The order of the pieces
- * is believed to be correct as given, however the sizes
- * of the gaps between them are based on estimates that have
- * provided by the submitter.

Qy	598	cacccggaccctgcacccccaggacacagctcgtctctgcactaccagccgctgcaccc	657
Db	225943	CACCCGGACCCCTGCACCCCGAGGACCAAGCTCGCTTCCTGCACCTACCAAGCCCTGC	225884
Qy	658	gcacccccggagccacaccgga--atccctggccccccagcccccgatgtgggctcctcgg	715
Db	225883	GCA-CCCCGGAGCCACCGGAATC	225885
Qy	716	accctctgagcatgtgtgggaacctccccagggccgaagccccagctacgctctcctgaagcc	775
Db	225824	NN	225756
Qy	776	agagggctttactatgacatctcctcttattattattagcttattatctattatttt	835
Db	225764	NNNGCGTGTTTACTATATGACATCTCCTCTTATTATTATTAGGTATTATCTATTATT	225705
Qy	836	ttattttcttacttgagataataaagagtccagagggaggagataagaatgagcatgtgt	895
Db	225704	TTTATTTTCTTACTTGAGATAATAAAGAGTTCACAGGAGGAGTAAAGAATGAGCATGTGT	225645
Qy	896	gagtgctcggaggagacatgagcagctgtttgtctcctcctggcccgacaaatccccctct	955
Db	225644	GAGTGTCTGAGGGAAGACATGGCAGCTGTGTGTCTTCCTTGCCCGCGGACAAACCCCTCT	225585
Qy	956	acacctccctcacgtgtgtccgagggctcctgggtctccacactgggctcactcttttcttt	1015
Db	225584	ACACCTCCCTCACGTGTCGAGGGTCCCTGGCTCCCACTGGGCTCAGCTTTTTCCTTTT	225525
Qy	1016	tcttttctttcttttttttttgacagcgagctcgtcgtcactccagccagccacagaca	1075
Db	225524	TCCTTTCTCTTTT-ATTTTTTTTGAGACGGAGTCTCGCTCTGTGTGACCCAGGCTGGAGTGCAGT	225466
Qy	1076	g 1076	
Db	225465	G 225465	
RESULT	8		
LOCUS	AC024740		
DEFINITION	AC024740	179538 bp DNA HTG 07-JUL-2000	
		Homo sapiens chromosome 19 clone RP11-801D6, WORKING DRAFT	
		SEQUENCE, 17 unordered pieces.	
ACCESSION	AC024740		
VERSION	AC024740.3	GI:85704005	
KEYWORDS	HTG; HTGS_PHASE1; HTGS DRAFT.		

FEATURES
source

BASE COUNT	ORIGIN
54671 a 58658 c 58905 g 54511 t	/clone_lib="CalTech human BAC library D"
	1204 others

```

Consensus quality: 173830 bases at least Q40
Consensus quality: 175557 bases at least Q30
Consensus quality: 176446 bases at least Q20
Insert size: 242000; agarose-fp
Insert quality: 177938; sum-of-contigs
Quality coverage: 5.32 in Q20 bases; agarose-fp
Quality coverage: 6.01 in Q20 bases; sum-of-contigs
-----
* NOTE: This is a 'working draft' sequence. It currently
* consists of 17 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

```

Contig	Contig of 1801 bp in length	Contig of unknown length	Contig of 1801 bp in length
1801	contig of 1801 bp in length		
1901	gap of unknown length		
1902	contig of 2740 bp in length		
4641	contig of unknown length		
4741	gap of unknown length		
4742	contig of 4938 bp in length		
9679	gap of unknown length		
9680	gap of unknown length		
9780	contig of 3613 bp in length		
13392	contig of unknown length		
13393	contig of 3672 bp in length		
13432	gap of unknown length		
17184	contig of unknown length		
17264	gap of unknown length		
21510	contig of 4246 bp in length		
21511	gap of unknown length		
21611	contig of 5479 bp in length		
27089	contig of unknown length		
27090	gap of unknown length		
27190	contig of 8447 bp in length		
35636	contig of unknown length		
35637	gap of unknown length		
45537	contig of 9801 bp in length		
45538	gap of unknown length		
45637	gap of unknown length		
56451	contig of 10814 bp in length		
56452	gap of unknown length		
56551	gap of unknown length		
66802	contig of 10251 bp in length		
66803	gap of unknown length		
79118	contig of 12216 bp in length		
79218	gap of unknown length		
94355	contig of 15137 bp in length		
94356	gap of unknown length		
94455	gap of unknown length		
111274	contig of 16819 bp in length		
111375	gap of unknown length		
130600	contig of 19226 bp in length		
130700	gap of unknown length		
150278	contig of 19578 bp in length		
150378	gap of unknown length		
179538	contig of 29160 bp in length		

FEATURES

```

location/gad11112
1. .179538
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="19"
/clone="RP11-801D6"
1. .1801
feature

```

misc_feature	1..1901	/note="assembly_name:Contig13"
misc_feature	1902..4641	/note="assembly_name:Contig14"
misc_feature	4742..9679	/note="assembly_name:Contig15"
misc_feature	9780..13392	/note="assembly_name:Contig16"
misc_feature	13493..17164	/note="assembly_name:Contig17"
misc_feature	17265..21510	/note="assembly_name:Contig18"
misc_feature	21611..27089	/note="assembly_name:Contig19"
misc_feature	27190..35636	/note="assembly_name:Contig20"
misc_feature	35737..45537	/note="assembly_name:Contig21"

[illegible]

RESULT	9
ABO25718	
LOCUS	ABO25718 633 bp mRNA
DEFINITION	Mus musculus mRNA for FGF-21, complete cds.
ACCESSION	ABO25718
VERSION	ABO25718.1 GI:9049446
KEYWORDS	FGF-21.
SOURCE	Mus musculus cDNA to mRNA.
ORGANISM	Mus musculus
	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

ORGANISM MUS MUSCULUS
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE 1 (sites)
AUTHORS Nishimura, T., Nakatake, Y., Konishi, M. and Itoh, N.
TITLE Identification of a novel FGF, FGF-21, preferentially expressed in the liver(1)
JOURNAL Biochim. Biophys. Acta 1492 (1), 203-206 (2000)
MEDLINE 20461777
REFERENCE 2 (bases 1 to 633)
AUTHORS Itoh, N.
TITLE Direct Submission
JOURNAL Submitted (02-APR-1999) to the DDBJ/EMBL/GenBank databases.
Nobuyuki Itoh, Kyoto University, Graduate School of Pharmaceutical Sciences, Department of Genetic Biochemistry, Yoshida-Shimoedachi, Sakyo, Kyoto, Kyoto 606-8501, Japan
(E-mail: itohnobu@pharm.kyoto-u.ac.jp, Tel:81-75-753-4540, Fax:81-75-753-4600)
FEATURES
source Location/Qualifiers
1..633
/organism="Mus musculus"
/db_xref="taxon:10090"
gene 1..633
/gene="FGF-21"
CDS 1..633
/gene="FGF-21"
/codon_start=1
/product="FGF-21"
/protein_id="BAA99416.1"
/db_xref="GI:9049447"
/translation="MEWMSRVGTGLWVLLAVLLGVYQAYPIPDSPILQFGGQ VRORYLTDQTEAHLREIDGTGVGAHRSPSELKALKPGVQILGVKASRF LCQPDGALYSPHFPEACSFRELLEDGYNVQSEAHGLPLRLPKQDPSNQDATSW GPPVRLPMGLLHEPDQDQAGFLPPEPPDVGSSDPLSMVPELQGRSPVAS"
BASE COUNT 136 a 198 c 173 g 126 t
ORIGIN
Query Match 33.98; Score 401.8; DB 94; Length 633;
Best Local Similarity 80.7%; Pred. NO. 5.1e-55;
Matches 469; Conservative 0; Mismatches 112; Indels 0; Gaps 0;
Qy 191 tgcctggctgtcttctgagcgtccaggcacacccccatccctgaactcagtcctc 250
Dy 53 TGC TGGCTGCTCTCTGCTGGGGTCTACCAAGCATACCCCATCCCTGACTCAGCCCCC 112
Qy 251 tcttgcgaattcggggcgaagtccggcagcgttacctctcacagatgctgcccagcaga 310
Dy 113 TCCTCCAGTTGGGGTCAAGTCGGGAGAGGTACCTCTACAGATGACGACACAGACA 172
Qy 311 cagaagccacctgagatcaggagagatggagcgtggggcgctgctgacccagagcc 370
Dy 173 CTGAAGCCACCTGGAGATCAGGAGGATGGAACAGTGGTAGGCGCAGCACACCGCAGTC 232
Qy 371 ccgaagctctcagctgaagccttggaagcggaggtattcaaatcttggaggtca 430
Dy 233 CAGAAAGTCTCTGAGCTCAAAAGCCTTGAAGCCAGGGGTCTATCAATCTCGGTGTCA 292
Qy 431 agacatcaggtctcctgctgcagcggcagatggggcctgtatgatgcctccactttg 490
Dy 293 AAGCTCTAGGTTCTTGGCAACAGCAGCATGAGCTCTCTATGATGCCCTCACTTTG 352
Qy 491 acctgaggcctgcagcttccggagctgctctttaggcagcagatacaatgtttaccagt 550
Dy 353 ATCTGAGGCTGCAGCTTCAGAGAACTGCTGCTGGGAGGACGGTTACAATGTGTACCA 412
Qy 551 ccgaagccacggcctcccgctgcacctgcagcgggaacagagtcacacacccggaccctg 610
Dy 413 CTGAAGCCCATGGCTCCCTCGCTGTGCTCAGAGGAGACTCCCAAAACAGGATGCAA 472
Qy 611 caccagacagcagctcgtctccactaccagcctgcccgcgcgcgcgcgcgcgcgcgcgc 670
Dy 473 CATCTGGGACCTGTGGCTTCTGTCCTGCCATCGAGGCGCTGCTCCACGAGCCCAAGACC 532
Qy 671 caccggaaatcctggccccccagccccccgagtgtgggctcctcggaaccctctgagcatgg 730

Db 533 AAGCAGGATTCCTGCCCCAGAGCCCCAGATGTGGCTCTCTGACCCCTGAGCATGG 592
Qy 731 tgggaccttccagggcgaagccccagctacgtctcctga 771
Dy 593 TAGAGCCTTTACAGGGCCGAGCCCGAGCTATGCGCTCTGA 633
RESULT 10
AF214655/c 9257 bp DNA ROD 23-MAR-2000
LOCUS Mus musculus alpha(1,2)fucosyltransferase FUT1 (Fut1) gene,
DEFINITION complete cds.
ACCESSION AF214655
VERSION AF214655.1 GI:7288502
KEYWORDS house mouse.
SOURCE Mus musculus
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 9257)
AUTHORS Domino, S.E. and Lowe, J.B.
TITLE Mus musculus alpha(1,2)fucosyltransferase FUT1 genomic sequence
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 9257)
AUTHORS Domino, S.E. and Lowe, J.B.
TITLE Direct Submission
JOURNAL Submitted (13-DEC-1999) HHMI, University of Michigan, 1150 W. Med.
Ctr. Dr., Ann Arbor, MI 48109-0650, USA
FEATURES
source Location/Qualifiers
1..9257
/organism="Mus musculus"
/strain="129/Ola"
/db_xref="taxon:10090"
/chromosome="7"
/map="23.2; between Klk1 and Ldh3"
/cell_line="E14"
/cell_type="ES"
/gene="Fut1"
/product="Fut1"
/note="glycosyltransferase; similar to the Mus musculus strain ICR sequences deposited at GenBank Accession Numbers Y09883 and AF113533; similar to the Mus musculus strain NIH Swiss sequence deposited at GenBank Accession Number U90553; similar to the Homo sapiens H blood group alpha(1,2)fucosyltransferase FUT1 sequences deposited at GenBank Accession Numbers M35531 and Z69587"
/codon_start=1
/protein_id="AAFA45145.1"
/db_xref="GI:7288503"
/translation="MWTSPRRQLGLTLLVLCVLSAGSFFHLLNGGNFRNGLILSVLC SDYHLKSPVAMVCLPHPLQTSNGSPSCSSLSGTWTITPGFRFGNQMGQYATLL ALAQLNGRAFIQPEMHAALAVFRI SILPILVDPEVSLTQWHLVLDHWMSEYSHLE DFLKLSGFGPCSWTFHHLRQIRREFTLHNHREGAQLLSGLRIGPAGTRPHFVGV VHVRRGDYLEVMPNWKGVGDRAVLAQAMDWFRARHKDPIFVVTSNGMKWCLNIDT SHGDVFNAGNCGECTPGKDFALLTQCNSHTINTICTGFWAAYLAGGDTVYLANFTLPD SEFLKIFRPEAFLEPMWVGINADSLQAQFDPWKPDSLFLKY"
polya_signal 8074..8079
BASE COUNT 2267 a 2195 c 2580 g 2215 t
ORIGIN
Query Match 18.3%; Score 217.2; DB 94; Length 9257;
Best Local Similarity 74.2%; Pred. NO. 1.2e-25;
Matches 307; Conservative 0; Mismatches 93; Indels 14; Gaps 2;


```

QY 720 tctgagcatggtggaactcccccagggccgaagcccccagctacgtcttcctga----- 771
Db 136767 CCTGAGCATGTTAGAGCGCTTTACAGGGCCGAAGCCCGAGCTATGCGTCTTGACTTTCCT 136826

QY 772 -agccagagcgtcttactatgacatcctcttatttatttatttatttatttatttattt 830
Db 136827 GAATCTAGGCGCTGTTCTTTTGGGTTTCACCTATTATTATACGGGTATTATTCTTATTT 136886

QY 831 attt-----ttttatttttcttctgagataataaagagttccagagagagat 879
Db 136887 ATTTATTATTAGTTTCTTTTCTTACTTGGAAATAAAGAGTCTGAAGAAATAAT 136941

RESULT 12
AK025772
LOCUS Homo sapiens 2550 bp mRNA PRI 29-SEP-2000
DEFINITION Homo sapiens CDNA: FLJ22119 fis, clone HEP18852.
ACCESSION AK025772
VERSION AK025772.1 GI:10438390
KEYWORDS oligo capping; fis (full insert sequence).
SOURCE Homo sapiens hepatoma cell_line:HepG2 CDNA to mRNA, clone_lib:HEP
clone:HEP18852.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (sites)
Kawabata,A., Hikiji,T., Kobatake,N., Inagaki,H., Ikema,Y.,
Okamoto,S., Okitani,R., Ota,T., Suzuki,Y., Obayashi,M., Nishi,T.,
Shibahara,T., Tanaka,T., Nakamura,Y., Isogai,T. and Sugano,S.
NEDO human cDNA sequencing project
Unpublished (2000)
2 (bases 1 to 2550)
Sugano,S., Suzuki,Y., Ota,T., Obayashi,M., Nishi,T., Isogai,T.,
Shibahara,T., Tanaka,T. and Nakamura,Y.
Direct Submission
Submitted (29-AUG-2000) to the DDBJ/EMBL/GenBank databases. Sumio
Sugano, Institute of Medical Science, University of Tokyo,
Laboratory of Genome Structure Analysis, Human Genome Center;
Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639, Japan
(E-mail:cdna@leims.u-tokyo.ac.jp, Tel:81-3-5449-5286,
Fax:81-3-5449-5416)
NEDO human cDNA sequencing project supported by Ministry of
International Trade and Industry of Japan; cDNA full insert
sequencing: Research Association for Biotechnology; cDNA library
construction, 3'- & 3'-end one pass sequencing: Department of
Virology and Human Genome Center, Institute of Medical Science,
University of Tokyo (partly supported by Science and Technology
Agency).
FEATURES
Location/Qualifiers
1..2550
/organism="Homo sapiens"
/db_xref="taxon:9606"
/cell_line="HepG2"
/cell_type="hepatoma"
/clone="HEP18852"
/clone_lib="HEP"
/notes="cloning vector pHE188FL3"
BASE COUNT 836 a 477 c 472 g 765 t
ORIGIN

Query Match 9.6%; Score 113.8; DB 89; Length 2550;
Best Local Similarity 87.9%; Pred No. 3.5e-09;
Matches 124; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

QY 1050 ctctgcactccagccagccagagcagattccattcctcaaaaaataaataataaa 1109
Db 2405 CACTGCACCTCCAGCGCTAGGTGACAGAGTGAGACTCCACTCACTAAAAA 2464

QY 1110 taaataataataataataataataataataataataataataataataataa 1169
Db 2465 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2524

```

```

QY 1170 aaaaaaaaaaaaaaaaaa 1190
Db 2525 AAAAAAAAAAAAAAAAAA 2545

RESULT 13
AC015686
LOCUS Homo sapiens 167403 bp DNA HTG 26-MAY-2000
DEFINITION Homo sapiens chromosome 11 clone RP11-15G21 map 11, WORKING DRAFT
SEQUENCE, 14 unordered pieces.
ACCESSION AC015686
VERSION AC015686.3 GI:8096826
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 167403)
Birren,B., Linton,L., Nusbaum,C. and Lander,E.
Homo sapiens chromosome 11, clone RP11-15G21
Unpublished
2 (bases 1 to 167403)
Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,M.,
Baldwin,J., Barna,N., Beckerly,R., Boguslavsky,L., Boukhgalter,B.,
Brown,A., Castle,A., Colangelo,M., Collins,S., Collamore,A.,
Cooke,P., DeArellano,K., Dewar,K., Domino,M., Donelan,L., Doyle,M.,
Ferrelira,P., FitzHugh,W., Forrest,C., Funke,R., Gage,D.,
Galagan,J., Gardyna,S., Grant,G., Hagos,B., Hearford,A., Horton,L.,
Howland,J.C., Johnson,R., Jones,C., Kann,L., Karatas,A., Klein,J.,
Lehoczky,J., Lieu,C., Locke,K., Macdonald,P., Marquis,N.,
McEwan,P., McGurk,A., McKernan,K., McLaughlin,J., Meldrim,J.,
Morrow,J., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P.,
Peterson,K., Pollara,V., Riley,R., Roy,A., Santos,R., Severy,P.,
Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J.,
Tesfaye,S., Tirrell,A., Vassiliev,H., Vo,A., Wheeler,J., Wu,X.,
Wyman,D., Ye.W.J., Zimmer,A. and Zody,M.
Direct Submission
TITLE JOURNAL
COMMENT
Submitted (17-NOV-1999) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On May 26, 2000 this sequence version replaced gi:6751811.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L1336
Center clone name: 15.G.21
----- Summary Statistics
Sequencing vector: M13; M77815; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 158650 bases at least Q40
Consensus quality: 162167 bases at least Q30
Consensus quality: 164010 bases at least Q20
Insert size: 170000; agarose-fp
Insert size: 166103; sum-of-contigs
Quality coverage: 4.7 in Q20 bases; agarose-fp
Quality coverage: 4.8 in Q20 bases; sum-of-contigs
-----
* NOTE: This is a 'working draft' sequence. It currently
* consists of 14 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 2189: contig of 2189 bp in length
* 2190 2289: gap of 100 bp

```

```
Query Match      9.2%; Score 109.6; DB 63; Length 167403;
Best Local Similarity 85.8%; Pred. No. 1.5e+08;
Matches 121: Conservative 0; Mismatches 20; Indels 0; Gaps 0
```

AF130087	2336 bp	mrna	PRI	01-DEC-2000
LOCUS				
DEFINITION	Homo sapiens clone FIB945 PRO2411	mrna, complete cds.		
ACCESSION	AF130087			



GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 6, 2001, 20:54:44 ; Search time 114.92 Seconds
(without alignments)
240.617 Million cell updates/sec

Title: US-09-391-861-2
Perfect score: 1116
Sequence: 1 MDSDETFEHSGLWVSLAG.....SSDPLSMVGPSQGRSPSYAS 209

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 425026 seqs, 132305027 residues
Total number of hits satisfying chosen parameters: 425026

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_16.*
1: sp_archaea.*
2: sp_bacteria.*
3: sp_fungi.*
4: sp_human.*
5: sp_invertebrate.*
6: sp_mammal.*
7: sp_mhc.*
8: sp_organelle.*
9: sp_phage.*
10: sp_plant.*
11: sp_rodent.*
12: sp_unclassified.*
13: sp_vertebrate.*
14: sp_virus.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1106	99.1	209	4 Q9NSA1	Q9nsal1 mus sapien
2	803.5	72.0	210	11 Q9JUN1	Q9jnl1 mus musculu
3	251.5	22.5	251	11 Q9EPC2	Q9epc2 mus musculu
4	228.5	20.5	251	4 Q9GZV9	Q9gzv9 homo sapien
5	218.5	19.6	227	13 Q9DDN0	Q9ddn0 gallus gall
6	171	15.3	206	13 Q9YGD8	Q9ygd8 oncorhynchu
7	168	15.1	196	13 Q9YH31	Q9yh31 notophthalm
8	165	14.8	212	11 Q9ESL9	Q9esh9 mus musculu
9	159.5	14.3	191	13 Q9DFC9	Q9dfc9 brachydanio
10	158	14.2	211	4 Q9NP95	Q9np95 homo sapien
11	137	14.1	212	11 Q9EST9	Q9est9 rattus norv
12	135	13.9	237	13 Q9IAI6	Q9iai6 gallus gall
13	153	13.7	245	13 Q9W6A2	Q9w6a2 gallus gall
14	150	13.4	208	13 Q9PVL1	Q9pvl1 xenopus lae
15	149	13.4	252	11 Q9O9G6	Q9o9g6 rattus norv
16	147	13.2	253	13 Q9IAI5	Q9iai5 gallus gall
17	146	13.1	192	11 Q9ERW3	Q9erw3 rattus norv
18	145	13.0	199	13 Q9IAI3	Q9iai3 gallus gall
19	144.5	12.9	207	11 Q9ERQ5	Q9erq5 mus musculu

20 144 12.9 212 13 042407
21 143.5 12.9 213 6 Q9NIB9
22 141 12.6 163 11 Q9JHL9
23 141 12.6 170 4 Q9HCT0
24 140.5 12.6 207 11 Q9ESL8
25 140 12.5 194 6 P79150
26 135 12.1 185 11 Q9ERN5
27 135 12.1 192 4 Q95830
28 134 12.0 194 6 Q9N198
29 131 11.7 162 11 Q9ESS2
30 131 11.7 243 13 Q9W6A1
31 130.5 11.7 181 13 Q9IAI7
32 128 11.5 106 6 Q9NIS8
33 125 11.2 146 13 Q07659
34 124.5 11.2 425 5 Q076831
35 123.5 11.1 770 5 P91672
36 123.5 11.1 770 5 Q9VDT9
37 123 11.0 101 13 P79706
38 123 11.0 127 4 Q99517
39 121 10.8 130 6 Q07767
40 121 10.8 196 4 P78443
41 118.5 10.6 1469 4 Q9HAR3
42 118.5 10.6 1474 4 Q94910
43 118 10.6 440 2 Q9EX20
44 117.5 10.5 1515 11 Q88917
45 117 10.5 108 6 Q9NIS7

ALIGNMENTS

RESULT 1
Q9NSA1
ID Q9NSA1 PRELIMINARY; PRT: 209 AA.
AC Q9NSA1;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE FGF-21.
GN FGF-21.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20461777; PubMed=10858549;
RA Nishimura T., Nakatake Y., Konishi M., Itoh N.;
RT "Identification of a novel FGF, FGF-21, preferentially expressed in the liver.";
RL Biochim. Biophys. Acta 1492:203-206(2000).
DR EMBL, AB021975; BAA99415.1; .
DR InterPro; IPR002209; .
DR InterPro; IPR002348; .
DR Pfam; PF00167; FGF; 1.
DR PRINTS; PR00263; HBGFFGF.
DR PRINTS; PR00262; ILIHGCF.
DR SMART; SM00442; FGF; 1.
SQ SEQUENCE 209 AA; 27925C52A0023823 CRC64;

Query Match 99.1%; Score 1106; DB 4; Length 209;
Best Local Similarity 99.5%; Pred. No. 2.9e-89;
Matches 208; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MDSDETFEHSGLWVSLAGLLGACQAHPIPDSPPLQFGQVQRQRYLYTDDAQQTEAH 60
Db 1 MDSDETFEHSGLWVSLAGLLGACQAHPIPDSPPLQFGQVQRQRYLYTDDAQQTEAH 60
QY 61 LEIRDGTGVGAADQSPESLLQLKALKPGVITQILGVKTSRFLCORPDGALYGSLLHFDEA 120
Db 61 LEIRDGTGVGAADQSPESLLQLKALKPGVITQILGVKTSRFLCORPDGALYGSLLHFDEA 120

Q9YGD8	ID	Q9YGD8	PRELIMINARY;	PRT;	206 AA.
AC	Q9YGD8;				
DT	01-MAY-1999	(TrEMBLrel. 10, Created)			
DT	01-MAY-1999	(TrEMBLrel. 10, Last sequence update)			
DE	01-MAR-2001	(TrEMBLrel. 16, Last annotation update)			
DE	FIBROBLAST GROWTH FACTOR 6-RELATED PROTEIN.				
GN	FGF6.				
OS	Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Actinopterygii; Neopterygii; Teleostei; Euteleostei;				
OC	Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.				
OX	NCBI_TaxID=8022;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=99096461; PubMed=9878802;				
RA	Rescan P.Y.				
RT	"Identification of a fibroblast growth factor 6 (FGF6) gene in a non-				
RT	mammalian vertebrate: continuous expression of FGF6 accompanies muscle				
RL	fiber hyperplasia."				
RL	Biochim. Biophys. Acta 1443:305-314(1998).				
DR	EMBL; Y16850; CAA76422.1; -				
DR	HSSP; P09038; 1BFF.				
DR	InterPro; IPR001064; -				
DR	InterPro; IPR002209; -				
DR	InterPro; IPR002348; -				
DR	Pfam; PF00167; FGF. 1.				
DR	PRINTS; PR00263; HBGFFGF.				
DR	PRINTS; PR00262; IL1HBGF.				
DR	ProDom; PD000831; -; 1.				
DR	PROSITE; PS00225; CRYSTALLIN_BETAGAMMA; UNKNOWN_1.				
DR	PROSITE; PS00247; HBGF_FGF. 1.				
DR	SMART; SM00442; FGF. 1.				
SQ	SEQUENCE 206 AA; 23375 MW; BB883328f17EB684 CRC64;				
Query Match	15.3%;	Score 171;	DB 13;	Length 206;	
Best Local Similarity	26.9%;	Pred. No. 1.6e-07;			
Matches 43;	Conservative 28;	Mismatches 57;	Indels 32;	Gaps	
Qy	10 HSGIWSVLGALLGACQAHPD-----SSPLQFGGQ-----	43			
Db	18 HWTLTAIVLLGVITGVSSYPISPTNTATLLEKRWETLFSRSLIGSEKSDLNWESDYL 77				
Qy	44 --VQRYLITDDAQTEAHLREIRDVGGAADQPSSLQLKALPGVIQILGVKTSR 100				
Db	78 LGIKRVRLYCNA--IGFHQLVDGRINGVHNENQYSLSIEITVERGVSVLYGRSEL 135				
Qy	101 FLCORPDGALYGLSHDPACSFRELLEDGYNYTQSEAH 140				
Db	136 EVAMNSRGRLYGTVPHDE-CKFRESMLPNNYAVESSVY 174				
RESULT 7					
Q9YH31	ID	Q9YH31	PRELIMINARY;	PRT;	196 AA.
AC	Q9YH31;				
DT	01-MAY-1999	(TrEMBLrel. 10, Created)			
DT	01-MAY-1999	(TrEMBLrel. 10, Last sequence update)			
DE	01-MAR-2001	(TrEMBLrel. 16, Last annotation update)			
DE	PUTATIVE FIBROBLAST GROWTH FACTOR-4.				
OS	Notoptthalmus viridescens (Eastern newt) (Pleurodeles waltl).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Amphibia; Batrachia; Caudata; Salamandroidea; Salamandridae;				
OC	Notoptthalmus.				
OX	NCBI_TaxID=8316;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RA	Wei Y.				
RT	"Putative Newt Fibroblast Growth Factor-4.";				
FL	Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.				
DR	EMBL; U76998; AAC98812.1; -				
DR	HSSP; P09038; 1BFF.				

```
DR InterPro; IPR001064; -.
DR InterPro; IPR002209; -.
DR InterPro; IPR002348; -.
DR Pfam; PF00167; FGF; 1
DR PRINTS; PR00263; HBGFFGF.
DR PRODOM; PD000831; -.
DR PROSITE; PS00225; CRYSTALLIN_BETAGAMMA; UNKNOWN_1.
DR PROSITE; PS00247; HBG_FGF; 1.
DR SMART; SM00442; FGF; 1.
SQ SEQUENCE 196 AA; 22033 MW; AC4688CD989C6EAF CRC64;

Query Match 15.1%; Score 168; DB 13; Length 196;
Best Local Similarity 28.9%; Pred. No. 2.8e-07;
Matches 44; Conservative 27; Mismatches 45; Indels 36; Gaps 5;

QY 17 VLAGLLGACQAHPTD--SSPLLQFGGQVRQRYLYTDD-----AQQTEA----- 59
DB 15 VLLGLLSGLARCLPMPSPGNGTLEWSWET----LYSOSLARLAGGQRTDAHRYGEYLLGI 70
QY 60 -----HLEIREDTGCGAADOQPESILQLKALKPGVIOILGVKTSRELCQR 105
DB 71 KRLRLRYNVGIGFHQLVLPDGRIGHMHSERYSLLEISPVGVCMFGVQSGLEFLAMN 130
QY 106 PDGALYGLSHFDPEACSFRELLLEDGYNVYQS 137
DB 131 SKGRLEFGSKYFSE-CKPKEMLLPNYAYES 161

RESULT 8
QY 9ESL9 PRELIMINARY; PRT; 212 AA.
AC 9ESL9;
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DE FIBROBLAST GROWTH FACTOR 20.
GN FGF20.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Itch N.;
RT "Mus musculus mRNA for FGF-20 (FGF20).";
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB049218; BAB16406.1; -.
SQ SEQUENCE 212 AA; 23659 MW; 174DBCE8915B69EF CRC64;

Query Match 14.8%; Score 165; DB 11; Length 212;
Best Local Similarity 33.5%; Pred. No. 5.7e-07;
Matches 54; Conservative 18; Mismatches 63; Indels 26; Gaps 6;

QY 32 PDSPLLQFGGQVRQRYLYTDDAQQTEAHLEIREDTGVGGA-ADQSPESILQLKALKPGV 90
DB 52 PGCSVELAHLHLIRRLQYLC----RTGHLQLLPDGTQGTQDHSFLGILEFISVAVGL 107
QY 91 IOILGVKTSRELCQRPDGLYGLSHFDPEACSFRELLLEDGYNVYQSAHGLPLHLPGNK 150
DB 108 VSIKGVDSGLYGLMMDKGLYSEKLTSE-CIFRQEQFENYNTYSSN-----IYKHGT 161
QY 151 -----SPHPAPRGPAR-----FLPLGLPPAPPE 176
DB 162 GRRYFVNLKDGTPRDGARSRRKROKFTFLRPVDPERVPE 202

RESULT 9
QY 9DFC9 PRELIMINARY; PRT; 191 AA.
AC 9DFC9;
```

```
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE FIBROBLAST GROWTH FACTOR 4 PRECURSOR.
OS Brachydanio rerio (Zebrafish) (Zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Osteichthyes; Ostariophysi;
OC Cypriniformes; Cyprinidae; Rasbora; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA Draper B.W.; Kimmel C.B.;
RT "FGF4 Expression is Associated with Numerous Developmentally Important
Signaling Centers During Zebrafish Embryogenesis.";
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF283555; AAG13950.1; -.
SQ SEQUENCE 191 AA; 21203 MW; D2B5F2FAD44B2289 CRC64;

Query Match 14.3%; Score 159.5; DB 13; Length 191;
Best Local Similarity 26.3%; Pred. No. 1.5e-06;
Matches 51; Conservative 27; Mismatches 69; Indels 47; Gaps 6;

QY 11 SGLWVSVLAGLLGACQAHPTD-----SSPLLQFGGQVRQ----- 46
DB 5 SALLPILVLGLMTSSVRCAPLPGGHSVPVRRWETLYSRSLARIPGCKRDISRDSYLG 64
QY 47 ----RYLYTDDAQQTEAHLEIREDTGVGGAADOQPESILQLKALKPGVIOILGVKTSRE 102
DB 65 IKRLRLRYNVG--IGFHQLVPGGKITGVHNRYSLLLEISPVGVVTLFGVRSGLFV 122
QY 103 QRPDGLYGLSHFDPEACSFRELLLEDGYNVYQSAHGLPLHLPG-----NKSP 152
DB 123 AMNSKGLYSGEQFTNE-CKFREKILLANNYAYESLAH-----PGMYIGLSKAGTKKG 175
QY 153 HRDPAPRGPARFLP 166
DB 176 NRVSTSTMTWTFPLP 189

RESULT 10
QY 9NP95 PRELIMINARY; PRT; 211 AA.
AC 9NP95;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE FGF-20 (FIBROBLAST GROWTH FACTOR 20) (FGF-20).
GN FGF-20.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE-20374469; PubMed-10913340;
RA Kirikawa H., Sagara N., Saitoh T., Tanaka K., Sekihara H.,
RA Shikawa K., Katoh M.;
RT "Molecular cloning and characterization of human FGF-20 on chromosome
8p21.3-p22.";
RL Biochem. Biophys. Res. Commun. 274:337-343(2000).
RN [2]
RP SEQUENCE FROM N.A.
RA Itoh N.;
RT "Human FGF-20.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB044277; BAB05633.1; -.
DR EMBL; AB030648; BAB03530.1; -.
DR InterPro; IPR002209; -.
DR InterPro; IPR002348; -.
DR Pfam; PF00167; FGF; 1.
DR PRINTS; PR00263; HBGFFGF.
DR PRINTS; PR00262; ILLHGF.
```



```

DR PROSITE: PS00247; HGF_FGF; 1.
DR SMART: SM00442; FGF; 1.
SQ SEQUENCE 211 AA; 23498 MW; AB04608C16060CC1 CRC64;

Query Match 14.2%; Score 158; DB 4; Length 211;
Best Local Similarity 33.1%; Pred. No. 2.3e-06;
Matches 53; Conservative 18; Mismatches 65; Indels 24; Gaps 6;

QY 32 PDSSPLLFQGGVQRVRYLYTDDAQTEAHLEIREDTGVGGA-ADQSPESLLQKALKPGV 90
DB 52 PGSAQLAHLGLRLRRQLYC-----RTGFHLQLPLDPSVQGTQDHSFLGILEFISVAVGL 107
QY 91 IQLGVKTSRFLCQPDGALYGLSHFDPEACSFRELLLEDGYNVYQSEAH-----GLPLH 145
DB 108 VSRIGVDSGLYGMNDKGLYSEKLTSE-CIFRQGFENWNTYSSNIYKHGDTGRRYF 166
QY 146 LPGNKSPHRDPAPRGPAR-----FLPLGLPPAPPE 176
DB 167 VALNK-----DGTFRDCAKSRKHQKTHFLPRVDPDPERVPE 202

RESULT 11
Q9EST9 PRELIMINARY; PRT; 212 AA.
AC Q9EST9;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE FGF-20.
GN FGF-20.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
[1]
RP SEQUENCE FROM N.A.
RC PubMed=11032730;
RX Tissue=ADULT BRAIN;
RA Ohmachi S., Watanabe Y., Mikami T., Kusu N., Ibi T., Akaike A.,
RA Itoh N.;
RA "FGF-20, a novel neurotrophic factor, preferentially expressed in the
RT substantia nigra pars compacta of rat brain.";
RL Biochem. Biophys. Res. Commun. 277:355-360(2000).
DR EMBL: AB020021; BAB13763.1; -.
SQ SEQUENCE 212 AA; 23537 MW; 4F958BEFE772B977 CRC64;

Query Match 14.1%; Score 157; DB 11; Length 212;
Best Local Similarity 33.8%; Pred. No. 2.8e-06;
Matches 54; Conservative 16; Mismatches 66; Indels 24; Gaps 6;

QY 32 PDSSPLLFQGGVQRVRYLYTDDAQTEAHLEIREDTGVGGA-ADQSPESLLQKALKPGV 90
DB 52 PGSAQLAHLGLRLRRQLYC-----RTGFHLQLPLDPSVQGTQDHSFLGILEFISVAVGL 107
QY 91 IQLGVKTSRFLCQPDGALYGLSHFDPEACSFRELLLEDGYNVYQSEAH-----GLPLH 145
DB 108 VSRIGVDSGLYGMNDKGLYSEKLTSE-CIFRQGFENWNTYSSNIYKHGDTGRRYF 166
QY 146 LPGNKSPHRDPAPRGPAR-----FLPLGLPPAPPE 176
DB 167 VALNK-----DGTFRDCAKSRKHQKTHFLPRVDPDPERVPE 202

RESULT 12
Q9IAI6 PRELIMINARY; PRT; 237 AA.
AC Q9IAI6;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE FIBROBLAST GROWTH FACTOR HOMOLOGOUS FACTOR 4 ISOFORM 1A (FRAGMENT).

```

```

GN FHF-4.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
[1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20112823; PubMed=10644718;
RA Munoz-Sanjuan I., Smallwood P.M., Nathans J.;
RT "Isoform Diversity among Fibroblast Growth Factor Homologous Factors
RT Is Generated by Alternative Promoter Usage and Differential
RT Splicing.";
RL J. Biol. Chem. 275:2589-2597(2000).
DR EMBL: AF199605; AAF31392.1; -.
DR InterPro: IPR002209; -.
DR InterPro: IPR002348; -.
DR Pfam: PF00167; FGF; 1.
DR PRINTS: PR00263; HBGFFGF.
DR PRINTS: PR00262; ILIHGFG.
DR ProDom: PD000831; -.
DR PROSITE: PS00247; HGF_FGF; 1.
DR SMART: SM00442; FGF; 1.
FT NON_TER 1
SQ SEQUENCE 237 AA; 26816 MW; F13076736548BB22 CRC64;

Query Match 13.9%; Score 155; DB 13; Length 237;
Best Local Similarity 29.3%; Pred. No. 4.8e-06;
Matches 61; Conservative 29; Mismatches 80; Indels 38; Gaps 9;

QY 24 GACQAHPIPOSSPLLFQGGVQRVRYLYTDDAQ-----QTEAHLEIREDTGVGGA 73
DB 27 GLCNGNLVDIFSKVRIFG--LKKRLRRQDPQLKGIIVTRYCQGVYVQLMHPDGLDGTK 84
QY 74 DQSPES-LLQLKALKPGVQIQLGVKTSRFLCQPDGALYGLSHFDPEACSFRELLLEDGY 132
DB 85 DSSNSTLFLNLPVGLRVVAIQGVKTLGYIALNNEGFLYTSFLTPE-CRKESVFENY 143
QY 133 NVYQS-----EAHGLPLH-----LPGNKSPPHRDPAPRGPARFLPLGLPPAPPEPP 178
DB 144 VIYSMLYRQESGRWFLGLNKGQGVKGNRVKTKTPA-----AHFLPKP-LEVAMYREP 198
QY 179 GILAPQPPDVGSSDPSLNVGSPQGRSPS 206
DB 199 SL-----HDIGETVPKAGVTPSKSTSAS 221

RESULT 13
Q9W6A2 PRELIMINARY; PRT; 245 AA.
AC Q9W6A2;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE FIBROBLAST GROWTH FACTOR 13 ISOFORM 1S (FIBROBLAST GROWTH FACTOR
DE HOMOLOGOUS FACTOR 2 ISOFORM IT+IS').
GN FGF13 OR FHF-2.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
[1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99063510; PubMed=9847253;
RA Munoz-Sanjuan I., Simandl B.K., Fallon J.F., Nathans J.;
RT "Expression of chicken fibroblast growth factor homologous factor
RT (FHF)-1 and of differentially spliced isoforms of FHF-2 during
RT development and involvement of FHF-2 in chicken limb development.";
RL Development 126:409-421(1999).
RN [2]
RP SEQUENCE FROM N.A.

```

<p>TISSUE=BRAIN;</p>					
RC	MEDLINE-20112823; PubMed=10644718;				
RX	Munoz-Sanjuan I., Smallwood P.M., Nathans J.;				
RA	"Isoform Diversity among Fibroblast Growth Factor Homologous Factors				
RT	Is Generated by Alternative Promoter Usage and Differential				
FT	Splicing.";				
RL	J. Biol. Chem. 275:2589-2597(2000).				
DR	EMBL; AF108755; AAD21576.1; -.				
DR	HSP; AF199611; AAF31398.1; -.				
DR	InterPro; IPR002209; -.				
DR	Pfam; PF00167; FGF; 1.				
DR	PRINTS; PR00263; HBGFFGF.				
DR	PRINTS; PR00262; ILIHGFG.				
DR	PROSITE; PS00247; HBGF_FGF; 1.				
DR	SMART; SM00442; FGF; 1.				
SQ	SEQUENCE 245 AA; 27605 MW; DA0DAFEDBA1B8F28 CRC64;				
Query Match	13.7%; Score 153; DB 13; Length 245;				
Best Local Similarity	29.8%; Pred. No. 7.5e-06;				
Matches	50; Conservative 23; Mismatches 67; Indels 28; Gaps 6;				
Qy	24 GACQAHPIDPSLLOFGGVQRORY-----LYTDDAQTEAHLEIREDTVGGAADQ 75 : : : : : : : : : : : : : : : :				
Dd	36 GSCDKNLNVSFKVLFSGKRRRPPQLKGIVTKLYSGYHLQLQAOGTDIGTKEE 95 : : : : : : : : : : : : : : : :				
Qy	76 -SPESLLQLKALKPGVIOLGVKTYSRFQCQRPDGALYGSLHFDPEACSFRELLLEDGYNV 134 : : : : : : : : : : : : : : : :				
Dd	96 DSSYTFLNFLIPGLRVVAIQGTVKLYLAMNSEGGYLVTSEHTPE-CFKKESIFENYYVT 154 : : : : : : : : : : : : : : : :				
Qy	135 Y-----QSEAHGLPLHL-----PCNKSPHRDPAPRGPARLP 168 : : : : : : : : : : : : : : : :				
Dd	155 YSMIYRQQSQGRGWYLGLENKEIMGNHVKKNP-----AHLPKP 198 : : : : : : : : : : : : : : : :				
RESULT 14					
ID Q9PVY1 PRELMINARY; PRT; 208 AA.					
AC Q9PVY1;					
DT 01-MAY-2000 (TREMBLrel. 13, Created)					
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)					
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)					
DE XFEGF-20.					
GN XFEGF-20.					
OS xenopus laevis (African clawed frog).					
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
CC Amphibia; Batrachia; Anura; Mesobatrachia; Piploidea; Pipidae;					
OX Xenopodinae; Xenopus.					
NCBI_TaxID=8355;					
[1]					
SEQUENCE FROM N.A.					
RX MEDLINE-99373151; PubMed=10441498;					
Koga C., Adati N., Nakata K., Mikoshiba K., Furuhata Y., Sato S.,					
Tai H., Sakaki Y., Kurokawa T., Shikokawa K., Yokoyama K.K.;					
"Characterization of a novel member of the FGF family, xFGF-20, in					
Xenopus laevis.";					
RL Biochem. Biophys. Res. Commun. 261:756-765(1999).					
DR EMBL; AB012615; BAA83474.1; -.					
DR HSP; P05230; 2AFG.					
DR InterPro; IPR002209; -.					
DR InterPro; IPR002348; -.					
Pfam; PF00167; FGF; 1.					
PRINTS; PR00263; HBGFFGF.					
PRINTS; PR00262; ILIHGFG.					
PROSITE; PS00247; HBGF_FGF; 1.					
SMART; SM00442; FGF; 1.					
SQ SEQUENCE 208 AA; 23438 MW; 268881D36E75704D CRC64;					
Query Match	13.4%; Score 150; DB 13; Length 208;				
Best Local Similarity	31.5%; Pred. No. 1.1e-05;				

Result No.	Query Match	Score	Query			DB	ID	Description
			Length	Length	Length			
1	273	24.5	216	1	FGF1_HUMAN	O95750	homo sapien	
2	206.5	18.5	218	1	FGF1_MOUSE	O35622	mus musculus	
3	179	16.0	245	1	FGF3_MOUSE	P05524	mus musculus	
4	177	15.9	206	1	FGF4_BOVIN	P18003	bos taurus	
5	176.5	15.8	208	1	FGF6_HUMAN	P10767	homo sapien	
6	174	15.6	187	1	FGFA_XENLA	P48805	xenopus lae	
7	170.5	15.3	208	1	FGF6_MOUSE	P21658	mus musculus	
8	170.5	15.3	239	1	FGF3_HUMAN	P11487	homo sapien	
9	168	15.1	266	1	FGF5_RAT	P48807	rattus norv	
10	165	14.8	194	1	FGF4_CHICK	P48804	gallus gall	
11	163.5	14.7	192	1	FGFB_XENLA	P48806	xenopus lae	
12	163.5	14.7	206	1	FGF4_HUMAN	P08620	homo sapien	
13	161	14.4	264	1	FGF5_MOUSE	P15656	mus musculus	
14	160.5	14.4	256	1	FGF3_BRARE	P48802	brachydanio	
15	155.5	13.9	155	1	FGF1_MESAU	P34004	mesocricetu	
16	155	13.9	247	1	FGF1_HUMAN	Q92915	homo sapien	
17	154.5	13.8	155	1	FGF1_MOUSE	P10935	mus musculus	
18	154	13.8	208	1	FGF9_HUMAN	P31371	homo sapien	
19	154	13.8	208	1	FGF9_RAT	P36364	rattus norv	
20	153.5	13.8	202	1	FGF4_MOUSE	P11403	mus musculus	
21	153.5	13.8	208	1	FGF9_MOUSE	P54130	mus musculus	
22	153	13.7	268	1	FGF5_HUMAN	P12034	homo sapien	
23	153	13.4	208	1	FGFA_HUMAN	O15520	homo sapien	
24	150	13.4	215	1	FGFA_RAT	P70492	rattus norv	
25	150	13.4	245	1	FGFD_MOUSE	P70377	mus musculus	
26	149	13.4	247	1	FGFE_MOUSE	P70379	mus musculus	
27	148	13.3	209	1	FGFA_MOUSE	O35565	mus musculus	
28	146.5	13.1	155	1	FGF1_HUMAN	P05230	homo sapien	
29	146	13.1	237	1	FGF3_XENLA	P36386	xenopus lae	
30	144.5	12.9	155	1	FGF1_BOVIN	P30968	bos taurus	
31	143.5	12.9	152	1	FGF1_PIG	P20002	sus scrofa	
32	143.5	12.9	207	1	FGF6_HUMAN	O43320	homo sapien	
33	142	12.7	220	1	FGF3_CHICK	P48801	gallus gall	

RESULT	1
FGFJ_HUMAN	
ID	FGFJ_HUMAN
STANDARD;	PRT; 216 AA.
AC	O95750;
DT	01-OCT-2000 (Rel. 40, Created)
DT	01-OCT-2000 (Rel. 40, Last sequence update)
DT	01-OCT-2000 (Rel. 40, Last annotation update)
DE	FIBROBLAST GROWTH FACTOR-19 PRECURSOR (FGF-19).
GN	FGF19.
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX	NCBI_TaxID=9606;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	TISSUE=Brain;
FX	MEDLINE=99132028; PubMed=9931477;
RA	Nishimura T., Utsunomiya Y., Hoshikawa M., Ohuchi H., Itoh N.;
FT	"Structure and expression of a novel human FGF, FGF-19, expressed in
RT	the fetal brain."
RL	Biochim. Biophys. Acta 1444:148-151(1999).

-!- TISSUE SPECIFICITY: EXPRESSED ONLY IN FETAL BRAIN.
-!- SIMILARITY: BELONGS TO THE HEPARIN-BINDING GROWTH FACTORS FAMILY.

This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See [http://www.isb-sib.ch/](http://www.isb-sib.ch/announce/) or send an email to license@isb-sib.ch).

CC	EMBL; AB018122; BAA75500.1; -	
DR	EMBL; AF1110400; AAD45973.1; -	
DR	MIM; 603891; -	
DR	HSP; P09038; 2BPH.	
DR	InterPro; IPR002209; -	
DR	InterPro; IPR002348; -	
DR	Pfam; PF00167; FGF; 1.	
DR	Pfam; PR00262; IL1HBGF.	
DR	PRINTS; PR00263; HGFCTGF.	
DR	PRINTS; PR00263; HGFCTGF.	
DR	PROSITE; PS00247; HGF_FGF; 1.	
KW	Growth factor; Signal.	
FT	SIGNAL	1 22
FT	CHAIN	23 216
FT		
CC		POTENTIAL. GROWTH FACTOR-19.
CC		FIBROBLAST

```
SQ SEQUENCE 216 AA; 24002 MW; E0BCBC9C220F9832 CRC64;
Query Match 24.5%; Score 273; DB 1; Length 216;
Best Local Similarity 36.8%; Pred. No. 9.9e-14;
Matches 78; Conservative 27; Mismatches 81; Indels 26; Gaps 9;

QY 11 SGLWVSVLGALLGACQAHPTDSSPLLOF--GGOVORYLYTDDAQ-QTEAHLEIREDDG 67
:||||:| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 14 AGLWLAV-AGRPPLA-----FSDAGPHVHYGWDPIRLRHLYTSGPHGLSCFLIRADG 66
| | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY 68 TVGGADQSPESLLQKALKPGVIOILGVKTSRFLCQPDGALYGLSLHFDPEACSFRELL 127
:||||:| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 67 VYDCARGSAHSLLEIKAVLTKVIAKGVHVSRYLCMGADKMQLLOYSEDCAFEEI 126
| | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY 128 LEDGYNVYQSEAHGLPLHLPNGKNSPHRDPAAPGPARFLP-----LGPLPAPPEPGI--- 180
|||||:| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 127 RPDGYNVYRSEKHRLPVSLSAKQ-RQLYKNRG---FLPLSHFLPMLPWPPEEPEDLRGH 182
| | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY 181 ----LAPQPPDVGGSDPLSMV-GPSQGRSPSY 207
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 183 LESDMFSPSLETDSMDPGLVLTGLAVRSPSF 214
| | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 2
FGFF_MOUSE
ID FGF3_MOUSE STANDARD; PRT; 218 AA.
AC O35622;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE FIBROBLAST GROWTH FACTOR-15 PRECURSOR (FGF-15).
GN FGF15.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97454242; PubMed=9310317;
RA McWhirter J.R., Goulding M., Weiner J.A., Chun J., Murre C.;
RT "A novel fibroblast growth factor gene expressed in the developing
RT nervous system is a downstream target of the chimeric homeodomain
RT oncoprotein E2A-Pbx1."
RL Development 124:3221-3232(1997).
CC -!- FUNCTION: MAY PLAY AN IMPORTANT ROLE IN REGULATING CELL DIVISION
CC AND PATTERNING WITHIN SPECIFIC REGIONS OF THE EMBRYONIC BRAIN,
CC SPINAL CORD AND SENSORY ORGANS.
CC -!- SUBCELLULAR LOCATION: SECRETED.
CC -!- TISSUE SPECIFICITY: EXPRESSED IN THE DEVELOPING BRAIN.
CC -!- SIMILARITY: BELONGS TO THE HEPARIN-BINDING GROWTH FACTORS FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AF007268; AAB63197.1; -.
CC DR MGD; MGI:1096383; Fgf15.
CC DR InterPro; IPR002209; -.
CC DR InterPro; IPR002348; -.
CC DR Pfam; PF00167; FGF; 1.
CC DR PRINTS; PR00262; ILLHGF.
CC DR PROSITE; PS00247; HBGFF_FGF; 1.
CC DR Growth factor; Signal.
CC FT CHAIN 1 25 POTENTIAL.
CC FT SIGNAL 26 218 FIBROBLAST GROWTH FACTOR-15.
CC SQ SEQUENCE 218 AA; 25236 MW; A96B0D771FE125A5 CRC64;
```

```
Query Match 18.5%; Score 206.5; DB 1; Length 218;
Best Local Similarity 33.8%; Pred. No. 8.1e-09;
Matches 53; Conservative 29; Mismatches 70; Indels 5; Gaps 4;

QY 13 LWSVSLAGLLGACQAHPTDSSPLLOF-GQV-RORYLYTDDAQTEAHLEIREDDGTVG 70
:||||:| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 19 LWLAVSRPL--AQSQSVSEDEPLFYLGKTRQLYLSAGPYVSNCFLRISDGSVD 76
| | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY 71 GADQSPESLLQKALKPGVIOILGVKTSRFLCQPDGALYGLSLHFDPEACSFRELL 130
:||||:| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 77 CEEDONRNLEFRAVALTKIAIKDVSSVRYLCMSADGKIYGLIRYSEEDCTPREMDCL 136
| | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY 131 GYNVYQSEAHGLPLHLPNGKNSPHRDPAAPGPARFLP 167
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 137 GYNVYRSMKHLHIIIFIQAK-PREQLQDQKPSNFIPV 172
| | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 3
FGF3_MOUSE
ID FGF3_MOUSE STANDARD; PRT; 245 AA.
AC P05524;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE INT-2 PROTO-ONCOGENE PROTEIN PRECURSOR (FIBROBLAST GROWTH FACTOR-3)
DE (FGF-3) (HBGF-3).
GN FGF3 OR FGF-3 OR INT-2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86247582; PubMed=3013624;
RA Moore R., Casey G., Brookes S., Dixon M., Peters G., Dickson C.;
RT "Sequence, topography and protein coding potential of mouse int-2: a
RT putative oncogene activated by mouse mammary tumour virus."
RL EMBO J. 5:919-924(1986).
RN [2]
RP SEQUENCE OF 1-73 FROM N.A.
RX MEDLINE=88296404; PubMed=2841106;
RA Smith R., Peters G., Dickson C.;
RT "Multiple RNAs expressed from the int-2 gene in mouse embryonal
RT carcinoma cell lines encode a protein with homology to fibroblast
RT growth factors."
RL EMBO J. 7:1013-1022(1988).
RN [3]
RP CHARACTERIZATION.
RX MEDLINE=91193291; PubMed=1964688;
RA Dickson C., Acland P., Smith R., Dixon M., Deed R., McAllan D.,
RA Walther W., Fuller-Pace F., Kiefer P., Peters G.;
RT "Characterization of int-2: a member of the fibroblast growth factor
RT family."
RL J. Cell Sci. Suppl. 13:87-96(1990).
CC -!- FUNCTION: COULD BE INVOLVED IN EAR DEVELOPMENT.
CC -!- INDUCTION: BY INTEGRATION OF MOUSE MAMMARY TUMOR VIRUS.
CC -!- SIMILARITY: BELONGS TO THE HEPARIN-BINDING GROWTH FACTORS FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; Y00848; CAA68767.1; -.
CC DR PIR; A23930; TVMST2.
CC DR HSSP; P09038; 2BFH.
CC DR MGD; MGI:95517; Fgf3.
CC DR InterPro; IPR002209; -.
CC DR InterPro; IPR002348; -.
CC DR Pfam; PF00167; FGF; 1.
```

```
DR PRINTS; PR00262; ILIHGFGF.  
DR PRINTS; PR00263; HBGFFGGF.  
DR PROSITE; PS00247; HBGF_FGF; 1.  
KW Transforming protein; Oncogene; Growth factor; Mitogen; Signal;  
FT SIGNAL. 1 17 POTENTIAL.  
FT CHAIN 18 245 INT-2 PROTO-ONCOGENE PROTEIN.  
FT CARBOHYD 65 65 N-LINKED (GLCNAC..).  
SQ SEQUENCE 245 AA; 27214 MW; 70D94FD6A783C79 CRC64;
```

Query Match 16.0%; Score 179; DB 1; Length 245;
Best Local Similarity 28.8%; Pred.No. 9.8e-07;
Matches 51; Conservative 30; Mismatches 78; Indels 18; Gaps

QY 41 GGQVRQRYLYTDDAQQTVAHLEIRDEGVVGAADQSPELLQLKALKPGVIQLLVKTSR 100
 || :||:|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
DB 40 GGAPRRKLVC-----ATKYHLQHLPSPGRVNSLSEAYSILLETAVEGVVAIKGLFSGR 95
 |::|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

QY 101 FLQRPDGALYGSLHFDPPEACSFRELLEDGYNYVQSEAHGLPLHLPKNKSPP--HRDPAP 158
 |::|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
DB 96 YLAMNKRGRLYSADYNAAE-CFEVERIHELGNITYASR-----LYRTSSSGPQAORQPGA 149
 |::|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

QY 159 RGP-----ARFLPLGLPPAPPPEGIIARPDPDVGSDDLPSMWGPSQGSRPSVAS 209
 ::|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
DB 150 QRPWTVSVNGKRPRRGFKTRTKQSKSLFLRVLGKHDMVMRLQQSQRAPGECS 206
 ::|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

RESULT 4
FGF4_BOVIN STANDARD; PRT; 206 AA.

ID FGF4_BOVIN AC P48803;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE FIBROBLAST GROWTH FACTOR-4 PRECURSOR (FGF-4) (HEPARIN SECRETORY DE TRANSFORMING PROTEIN) (HST) (HBGF-4).
GN FGF4 OR HST.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RS SEQUENCE FROM N.A.
RC TISSUE=Thymus;
RX MEDLINE=96032369; PubMed=7557455;
RA Yu J.-C., Deseabra A.J., Wang L.M., Fleming T.P., Chedid M.,
RA Mikl T., Heidaran M.A.;
RT "An unexpected transforming gene in calf-thymus carrier DNA: bovine hst."
RL Gene 162:333-334(1995).

-- -- SIMILARITY: BELONGS TO THE HEPARIN-BINDING GROWTH FACTORS FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation - European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/ or send an email to licensel@isb-sib.ch).
CC -----
CC EMBL: U15969; AAA91622.1; -.
DR DR HSSP: P05038; 1BFf
DR DR InterPro: IPR002209; -.
DR DR Pfam: PF00167; FGF; 1.
DR DR PRINTS; PR00262; ILIHGFGF.
DR DR PRINTS; PR00263; HBGFFGGF.
DR DR PROSITE; PS00247; HBGF_FGF; 1.
KW Transformed protein; Oncogene; Growth factor; Mitogen; Signal.
FT SIGNAL 1 ? POTENTIAL.
FT CHAIN ? 206 FIBROBLAST GROWTH FACTOR-4.


```

RESULT      8
FGF3_HUMAN
ID   FGF3_HUMAN      STANDARD;          PRT;   239 AA.
AC   P11487;
DT   01-OCT-1989 (Rel. 12, Created)
DT   01-OCT-1989 (Rel. 12, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   INT-2 PROTO-ONCOGENE PROTEIN PRECURSOR (FIBROBLAST GROWTH FACTOR-3)
DE   (FGF-3) (HBGF-3).
DN   FGF3 OR INT2.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RT   TISSUE=Placenta;
RX   MEDLINE=89239468; PubMed=24770007;
RA   Brooks S., Smith R., Casey G., Dickson C., Peters G.;
RT   "sequence organization of the human int-2 gene and its expression in
RT   teratocarcinoma cells.";
RL   Oncogene 4:429-436(1989).
CC   -|- FUNCTION: COULD BE INVOLVED IN EAR DEVELOPMENT.
CC   -|- SIMILARITY: BELONGS TO THE HEPARIN-BINDING GROWTH FACTORS FAMILY.
CC   -----
CC   THIS SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announcement).
CC   or send an email to license@isb-sib.ch.
CC   -----
DR   EMBL; X14445; CAA32615.1; -.
DR   PIR; S04742; S04742.

```



```
SQ SEQUENCE 192 AA; 21903 MW; 2B01B0BB8824E3B3 CRC64;

Query Match 14.7%; Score 163.5; DB 1; Length 192;
Best Local Similarity 32.4%; Pred. No. 1e-05;
Matches 36; Conservative 26; Mismatches 44; Indels 5; Gaps 3;

QY 60 HLEIREDTGVTGGADQSPESLLQKALKPGVIOILGVKTSRFLCORPDGALYGLSHFDPE 119
DQ 81 HIQVLPDGRINGMHNRYSLLETSPEVGVWSLYGKISAMFVAMNAKAGLYGSRVFN-E 139
QY 120 ACSFRELLLEDGYNVQSEAH-GLPLHLPGN---KSPHRDPAPRGPARFLP 166
DQ 140 ECKFKETLLPNYNAYESRYPGMIALGKNGRTKKNRVSPVTMTLTHFLP 190

RESULT 12
FGF4_HUMAN STANDARD; PRT; 206 AA.
AC P08620;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-AUG-1988 (Rel. 08, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE FIBROBLAST GROWTH FACTOR-4 PRECURSOR (FGF-4) (HEPARIN SECRETORY
DE TRANSFORMING PROTEIN) (HST-1) (HST) (TRANSFORMING PROTEIN KS3) (HBGF-
DE 4).
GN FGF4 OR HST OR HSTF1 OR KS3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88041096; PubMed=2959959;
RA Yoshida T., Miyagawa K., Odagiri H., Sakamoto H., Little P.F.R.,
RA Terada M., Sugimura T.;
RT "Genomic sequence of hst, a transforming gene encoding a protein
RT homologous to fibroblast growth factors and the int-2-encoded
RT protein.;"
RL Proc. Natl. Acad. Sci. U.S.A. 84:7305-7309(1987).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=87204251; PubMed=2953031;
RA Taira M., Yoshida T., Miyagawa K., Sakamoto H., Terada M.,
RA Sugimura T.;
RT "cDNA sequence of human transforming gene hst and identification of
RT the coding sequence required for transforming activity.;"
RL Proc. Natl. Acad. Sci. U.S.A. 84:2980-2984(1987).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=87301716; PubMed=2957062;
RA Dell'I Bovi P., Curatola A.M., Kern F.G., Greco A., Ittmann M.,
RA Basilio C.;
RT "An oncogene isolated by transfection of Kaposi's sarcoma DNA encodes
RT a growth factor that is a member of the FGF family.;"
RL Cell 50:729-737(1987).
CC -1- FUNCTION: CAN TRANSFORM NIH 3T3 CELLS FROM A HUMAN STOMACH TUMOR
CC (HST) AND FROM KAPOSI'S SARCOMA (KS3). IT HAS A MITOGENIC
CC ACTIVITY.
CC -1- SIMILARITY: BELONGS TO THE HEPARIN-BINDING GROWTH FACTORS FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DQ EMBL; J02986; AAB59555.1; -
DQ EMBL; M17446; AAB59473.1; -
DQ PIR; A28417; TVHUHS.
DQ HSP; P09038; 1BFF.

MIM; 164980; -
DR InterPro; IPR002209; -
DR InterPro; IPR002348; -
DR Pfam; PF00167; FGF; 1.
DR PRINTS; PR00262; ILIHGFG.
DR PRINTS; PR00263; HBGF-FGF.
DR PROSITE; PS00247; HBGF_FGF; 1.
KW Transforming protein; Oncogene; Growth factor; Mitogen; Signal.
FT SIGNAL 1 ? POTENTIAL.
FT CHAIN 1 ? 206 FIBROBLAST GROWTH FACTOR-4.
SQ SEQUENCE 206 AA; 22047 MW; C7FD54A0272A1569 CRC64;

Query Match 14.7%; Score 163.5; DB 1; Length 206;
Best Local Similarity 36.9%; Pred. No. 1e-05;
Matches 41; Conservative 19; Mismatches 46; Indels 5; Gaps 3;

QY 60 HLEIREDTGVTGGADQSPESLLQKALKPGVIOILGVKTSRFLCORPDGALYGLSHFDPE 119
DQ 95 HLQALPDGRIGGAHADTRDSLLELSPVERGVVIFGVASRFFVAMSSKGLYGSPTFTDE 154
QY 120 ACSFRELLLEDGYNVQSEAH-GLPLHLPGN---KSPHRDPAPRGPARFLP 166
DQ 155 -CTFKETLLPNYNAYESKYKYPGMEIALSKNGTKKKNRVSPVTMKVTHFLP 204

RESULT 13
FGF5_MOUSE STANDARD; PRT; 264 AA.
AC P15656;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE FIBROBLAST GROWTH FACTOR-5 PRECURSOR (FGF-5) (HBGF-5).
GN FGF5 OR FGF-5.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90201563; PubMed=2318343;
RA Hebert J.M., Basilio C., Goldfarb M., Haub O., Martin G.R.;
RT "Isolation of cDNAs encoding four mouse FGF family members and
RT characterization of their expression patterns during embryogenesis.;"
RL Dev. Biol. 138:454-463(1990).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=C57BL/6;
RX MEDLINE=91045929; PubMed=1700424;
RA Haub O., Drucker B., Goldfarb M.;
RT "Expression of the murine fibroblast growth factor 5 gene in the
RT adult central nervous system.;"
RL Proc. Natl. Acad. Sci. U.S.A. 87:8022-8026(1990).
CC -1- SIMILARITY: BELONGS TO THE HEPARIN-BINDING GROWTH FACTORS FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DQ EMBL; M30643; AAA96698.1; -
DQ EMBL; M37823; AAB02660.1; -
DQ EMBL; M37821; AAB02660.1; JOINED.
DQ EMBL; M37822; AAB02660.1; JOINED.
DQ EMBL; M37821; AAB02659.1; ALT_SEQ.
DQ PIR; A36207; A36207.
DQ PIR; B37360; B37360.
DQ HSP; P09038; 1BFC.
DQ MGI; MGI:95519; Fgf5.
```

[illegible]

Best Local Similarity 35.0%; Pred. No. 3.2e-05;
Matches 48; Conservative 12; Mismatches 62; Indels 15; Gaps 5;

QY	41	GGQVRQRYLYTDDAQTEAHLEIREDTVGGAADOSPESL-LQKALKPGVIQILGVKTS	99
Db	21	GNVKKPKLLYCSNGGH---FLRLPDGTVGTRDRSDQHILQLSAESAGEVIKGTETG	77
QY	100	RLCQRPDGALYGLHFDPEACSFRELLEDGYNVYQSEAHGLPLHLFCNKSPPHRDPAPR	159
Db	78	QYLAMDTDGLLYGS-QTPNEECFLERLEENHYNTYTSKKHAEKNWFVGLKK--NGSCKR	134
QY	160	GPAP-----FLPLP	168
Db	135	GPRTHYGQKAILFLPLP	151

Search completed: August 6, 2001, 21:09:57
Job time: 723 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 6, 2001, 20:49:59 ; Search time 67.44 Seconds
(without alignments)
236.069 Million cell updates/sec

Title: US-09-391-861-2
Perfect score: 1116
Sequence: 1 MDSDETFEHSGLMWSVLG.....SSDPLSMVGPSQGRSPSYAS 209

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues
Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_68:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	251.5	22.5	251	3	JC7513
2	179	16.0	245	1	TMVST2
3	176.5	15.8	208	2	S20102
4	174	15.6	187	2	S23595
5	173	15.5	206	2	JC4268
6	170.5	15.3	208	2	SL1492
7	170.5	15.3	239	1	S04742
8	168	15.1	266	2	S68144
9	165	14.8	194	2	I50710
10	163.5	14.7	192	2	S54407
11	163.5	14.7	206	1	TVHUS
12	161	14.4	264	2	A36207
13	160.5	14.4	256	2	JC4627
14	158	14.2	211	2	JC7353
15	157	14.1	212	3	JC7511
16	155.5	13.9	155	1	A60721
17	154.5	13.8	155	2	S04147
18	154.5	13.8	155	2	D37360
19	154	13.8	208	2	S66486
20	154	13.8	208	2	A48137
21	153.5	13.8	202	1	TMVSHS
22	150	13.4	208	2	JC7082
23	148.5	13.3	267	1	TVHUF5
24	146.5	13.1	155	1	A33665
25	146	12.9	155	1	S39582
26	144.5	12.9	155	1	GKBOA
27	143.5	12.9	152	2	JH0476
28	143.5	12.9	207	2	JC5941
29	142	12.7	194	2	S26049

30 142 12.7 220 2 I50588 fibroblast growth
31 141 12.6 194 2 S49501 keratinocyte growt
32 140 12.5 194 2 I48610 keratinocyte growt
33 139.5 12.5 207 2 JC5940 fibroblast growth
34 139 12.5 194 1 A36301 fibroblast growth
35 138 12.4 189 2 A48834 basic fibroblast g
36 135 12.1 155 1 A40117 basic fibroblast g
37 131.5 11.8 155 2 JH0055 acidic fibroblast
38 127.5 11.4 155 2 A60130 acidic fibroblast
39 127 11.4 164 2 S31622 basic fibroblast g
40 122 10.9 154 2 A31674 basic fibroblast g
41 122 10.9 154 2 C37360 basic fibroblast g
42 122 10.9 168 2 JG0184 fibroblast growth
43 121 10.8 137 2 I46711 fibroblast growth
44 121 10.8 146 1 S00185 basic fibroblast g
45 121 10.8 157 1 GKB0B basic fibroblast g

ALIGNMENTS

RESULT 1
JC7513
fibroblast growth factor-23 - mouse
C:Species: Mus musculus (house mouse)
C:Date: 31-Mar-2001 #sequence_revision 31-Mar-2001 #text_change 31-Mar-2001
C:Accession: JC7513
R:Yamashita, T.; Yoshioka, M.; Itoh, N.
Biochem. Biophys. Res. Commun. 277, 494-498, 2000
A:Title: Identification of a novel fibroblast growth factor, FGF-23, preferentially e
A:Reference number: JC7513; MUID:20490027
A:Contents: Embryo
A:Accession: JC7513
A:Molecule type: mRNA
A:Residues: 1-251 <YAM>
A:Cross-references: DDBJ:AB037889
C:Comment: This factor, a secreted protein, acts on proximal cells and plays roles in
C:Genetics:
A:Gene: fgf-23
C:Keywords: nucleus

Query Match 22.5%; Score 251.5; DB 3; Length 251;
Best Local Similarity 32.1%; Pred. No. 1.9e-12;
Matches 76; Conservative 23; Mismatches 85; Indels 53; Gaps 9;
Qy 12 GLWVSVLAGLLGACQ---AHPIDPSPLL--QFGGVQRQRYLYTDDAQQTFAHLEIREED 66
Db 3 GTCLRLVGVLCVCSLGTARAYPDTSPLLGNNGLT---HLVTATA-RTSYHLQIHRD 58
Qy 67 GTVGAADSPESLLQALKAPGVIOILGVKTSRFLCQRPDPCALYGLSHFDPEACSFREL 126
Db 59 GHVDGTPHQTITYSALMITSEDAGSVITGAMTRFLCMLDHLGNIFGSLHFSPECKRFQW 118
Qy 127 LLEDGYNVQSEAHGLPHL-----PGNKS----- 152
Db 119 TLENGYDVLQSKHHVLSGLRAKRIQPGTNPFPFQFLARRNEVLLHFYIVRPRHT 178
Qy 153 ---HNDPAPRGAPREL-PLPGLFPAP----PEPPGILAPQPPDVGSSDPLSMVGPSQG 202
Db 179 RSAEDPPERDPLNVLKPRPRATPVVSCRELPSAERGPP---AASDPLGLVLRGRG 232

RESULT 2
TMVST2
transforming protein (int-2) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 31-Dec-1989 #sequence_revision 31-Dec-1989 #text_change 18-Jun-1999
C:Accession: A23930; S08157
R:Moore, R.; Casey, G.; Brookes, S.; Dixon, M.; Peters, G.; Dickson, C.
EMBO J. 5, 919-924, 1986
A:Title: Sequence, topography and protein coding potential of mouse int-2: a putative
A:Reference number: A23930; MUID:86247582

Db 139 IAMNSKGRLYTTPSFHDE-CKFRETLLPNNYAYESDLY 176

Db 123 AVSOGIVGIRGVSNKFLAMSKKGLHASAKFTDD-CKFRERFOENSNTYASAIHRTEK 181
QY 141 -GLPLHLPGNKSPHRDPAPRG-----PARFLP-----LPGLP-----PAPPEPP 178
Db 182 TGREWYVALNK---RGKAKRGSPRVKQHQVSTHFLPRFKQSEQPELSFTVTVPKPKPP 238
QY 179 GILAPQPPDVGSSDPLSMVGPQSGRSPS 206
Db 239 ---RPWPKPV-----PLS---PSR-RSPS 255

RESULT 9
I50710
fibroblast growth factor 4 - chicken
C:Species: Gallus gallus (chicken)
C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 16-Jul-1999
C:Accession: S78506; S50858; I50710
R:Niswander, L.
submitted to the EMBL Data Library, September 1994
A:Reference number: S78506
A:Accession: S78506
A:Molecule type: DNA
A:Residues: 1-194 <NS>
A:Cross-references: EMBL:U14654; NID:9609347; PIDN:AAA58706.1; PID:9609348
R:Niswander, L.; Jeffrey, S.; Martin, G.R.; Tickle, C.
Nature 371, 609-612, 1994
A:Title: A positive feedback loop coordinates growth and patterning in the vertebrate limb
A:Reference number: I50710; MUID:95021713
A:Accession: S50858
A:Status: nucleic acid sequence not shown
A:Molecule type: DNA
A:Residues: 1-136, 'Q', 137-194, 'I' <NIW>
A:Cross-references: EMBL:U14654; NID:9609347; PIDN:AAA58706.1; PID:9609348
C:Genetics:
A:Gene: FGF4
C:Superfamily: fibroblast growth factor
C:Keywords: growth factor; transforming protein

Query Match 14.8%; Score 165; DB 2; Length 194;
Best Local Similarity 27.3%; Pred. No. 6.6e-06;
Matches 53; Conservative 29; Mismatches 68; Indels 44; Gaps 7;

QY 11 SGLWVSVALGILL-GACQAHPTP-----DSSP 36
Db 5 ALLPALLGLLWPCAVGRPPPGPLPQPRQRWDALFARSVARLPAERDRAARDGY 64
QY 37 LQFGQGVQRVLYTDDAQQTEAHLEIREDTGTVGGADQSPESLLQKALKPGVQIILGV 96
Db 65 LL--GYKRLRLRYCNVG--IGFHIQVLPDGRIDGIHSENYRSLLEISPVGVVSGV 119
QY 97 KTSRFLCQPDGALYGLHFDPEACSFRELLEDGYNVYQSEAH-GLPLHLPGN---KSP 152
Db 120 RSLGVFAMNSKGLYGSTHVNDE-CKFKEILLPNNNAYESRYIFPGMYIALSKNGRTKK 178
QY 153 HRDPAPRGPARFLP 166
Db 179 NKVSPMTVTHFLP 192

RESULT 10
S54407
embryonic fibroblast growth factor II - African clawed frog
C:Species: Xenopus laevis (African clawed frog)
C:Date: 06-Sep-1996 #sequence_revision 13-Mar-1997 #text_change 17-Mar-2000
C:Accession: S54407
R:Isaacs, H.V.; Tannahill, D.; Slack, J.M.W.
Development 114, 711-720, 1992
A:Title: Expression of a novel FGF in the Xenopus embryo. A new candidate inducing factor
A:Reference number: S23595; MUID:92315916
A:Accession: S54407
A:Status: preliminary
A:Molecule type: mRNA

A:Residues: 1-192 <ISA>
A:Cross-references: EMBL:X62594; NID:g840919; PIDN:CAA44480.1; PID:g840920
C:Superfamily: fibroblast growth factor

Query Match 14.7%; Score 163.5; DB 2; Length 192;
Best Local Similarity 32.4%; Pred. No. 8.5e-06;
Matches 36; Conservative 26; Mismatches 44; Indels 5; Gaps 3;

QY 60 HLEIREDTGTVGGADQSPESLLQKALKPGVQIILGVKTSRFLCQPDGALYGLHFDPE 119
Db 81 HIQVLPDGRINGMHNENRYSLLEISPEVGVWSLYGIKSAMFVAMNAKGLYGSRYFN-E 139
QY 120 ACSFRELLEDGYNVYQSEAH-GLPLHLPGN---KSPHRDPAPRGPARFLP 166
Db 140 ECAFKEILLPNNNAYESRYKYPGMYIALGKNGRTKKGNRVSPMTVTHFLP 190

RESULT 11
TVHUHS
fibroblast growth factor 4 - human
N:Alternate names: heparin secretory transforming protein 1; Kaposi sarcoma oncogene;
C:Species: Homo sapiens (man)
C:Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 18-Jun-1999
C:Accession: A28417; A29876; A29649
R:Yoshida, T.; Miyagawa, K.; Odagiri, H.; Sakamoto, H.; Little, P.F.R.; Terada, M.; S
Proc. Natl. Acad. Sci. U.S.A. 84, 7305-7309, 1987
A:Title: Genomic sequence of hst, a transforming gene encoding a protein homologous t
A:Reference number: A28417; MUID:88041096
A:Accession: A28417
A:Molecule type: DNA
A:Residues: 1-206 <YOS>
A:Cross-references: DDBJ:J02986; NID:g184430; PIDN:AAB59555.1; PID:g386788
R:Taira, M.; Yoshida, T.; Miyagawa, K.; Sakamoto, H.; Terada, M.; Sugimura, T.
Proc. Natl. Acad. Sci. U.S.A. 84, 2980-2984, 1987
A:Title: cDNA sequence of human transforming gene hst and identification of the codin
A:Reference number: A29876; MUID:87204251
A:Accession: A29876
A:Molecule type: mRNA
A:Residues: 1-206 <TAI>
A:Cross-references: GB:J02986; GB:M16338; NID:g184430; PIDN:AAB59555.1; PID:g386788
R:Belli Bovi, P.; Curatola, A.M.; Kern, F.G.; Greco, A.; Ittmann, M.; Basilico, C.
Cell 50, 729-737, 1987
A:Title: An oncogene isolated by transfection of Kaposi's sarcoma DNA encodes a growt
A:Reference number: A29649; MUID:87301716
A:Accession: A29649
A:Molecule type: mRNA
A:Residues: 1-206 <BOV>
A:Cross-references: GB:M17446; NID:g186785; PIDN:AAA59473.1; PID:g307092
C:Comment: This protein is an oncogene for Kaposi's sarcoma. It is homologous to the
C:Genetics:
A:Gene: GDB:FGF4; HSTF1
A:Cross-references: GDB:120066; OMIM:164980
A:Map position: 11q13.3-11q13.3
A:Introns: 114/1; 148/3
C:Superfamily: fibroblast growth factor
C:Keywords: growth factor; Kaposi sarcoma; transforming protein

Query Match 14.7%; Score 163.5; DB 1; Length 206;
Best Local Similarity 36.9%; Pred. No. 9.2e-06;
Matches 41; Conservative 19; Mismatches 46; Indels 5; Gaps 3;

QY 60 HLEIREDTGTVGGADQSPESLLQKALKPGVQIILGVKTSRFLCQPDGALYGLHFDPE 119
Db 95 HQALPDGRTGGYAHADTRDLSLEISPEVGVWSIFGVSRFFVAMSSKGLYGSFFTTDE 154
QY 120 ACSFRELLEDGYNVYQSEAH-GLPLHLPGN---KSPHRDPAPRGPARFLP 166
Db 155 -CTFKEILLPNNNAYESRYKYPGMYIALGKNGRTKKGNRVSPMTMKVTHFLP 204

RESULT 12

[illegible]

A:Reference number: JJC/353
A:Accession: JJC7353
A:Molecule type: mRNA
A:Residues: 1-211 <KIR>
A:Cross-references: DDBJ:AB044277
C:Comment: This factor is involved in physiological and pathological processes, playi
C:Genetics:
A:Gene: fgf-20
A:Map position: 8p21.3-8p22
C:Superfamily: fibroblast growth factor
C:Keywords: angiogenesis; carcinogenesis

Query Match	14.2%	Score 158;	DB 2;	Length 211;
Best Local Similarity	33.1%	Pred. No. 2.5e-05;		
Matches 53;	Conservative 18;	Mismatches 65;	Indels 24;	Gaps 6;

[illegible]

RESULT 15
JC7511
fibroblast growth factor-20 - rat
C/Species: Rattus norvegicus (Norway rat)
C/Date: 31-Mar-2001 #sequence_revision 31-Mar-2001 #text_change 31-Mar-2001
C/Accession: JC7511
A/Olmachi, S.; Watanabe, Y.; Mikami, T.; Kusu, N.; Ibi, T.; Akaike, A.; Itoh, N.
Biochem. Biophys. Res. Commun. 277, 355-360, 2000
A/Title: FGF-20, a novel neurotrophic factor, preferentially expressed in the substan
A/Reference number: JC7511; MUID:20490008
A/Contents: Brain
A/Accession: JC7511
A/Molecule type: DNA
A/Residues: 1-212 <OHM>
A/Cross-references: DDBJ:AB020021

C;Genetics:
A;Gene: fqf-20

Db 40 GGAPRRKLYC-----ATKYHLQHPGSRVNGSLNSAYSILLETAVGVVAIKLFSGR 95
QY 101 FLCQPDGALYGLHFDPEACSFRELLLEDGYNVYQSEAHGLPLHLPGNKSP--HRDPAP 158
Db 96 YLAMNKRGLYASDHYNAE-CEVERIHGELGYNTYASR-----LYRTGSSGPGAQRPQGA 149
QY 159 RGP-----ARFLPLGLPPAPPEPGIILAPQPPDVGSSDPLSMVGPQSGRSPSYAS 209
Db 150 QRPWTVSVNGKGRPRGRFTRTKQSSLFPLRVLGHKDHEMWRLQLQSSQPRAPGEGS 206

RESULT 2

US-08-867-471-11
; Sequence 11, Application US/08867471
; Patent No. 5872226
; GENERAL INFORMATION:
; APPLICANT: Nathans, Jeremy
; APPLICANT: Smallwood, Philip M.
; APPLICANT: Macke, Jennifer P.
; TITLE OF INVENTION: FIBROBLAST GROWTH FACTOR HOMOLOGOUS
; TITLE OF INVENTION: FACTOR-1 (FHF-1) AND METHODS OF USE
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/867.471
; FILING DATE: 02-JUN-1997

CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/439,725
; FILING DATE: 12-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Haile, Lisa A.
; REGISTRATION NUMBER: 38,347
; REFERENCE/DOCKET NUMBER: 07265/047001

TELEPHONE: 619/678-5070
; TELECOMMUNICATION INFORMATION:
; TELEFAX: 617/678-5099
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 245 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-867-471-11

Query Match 16.0%; Score 179; DB 2; Length 245;
Best Local Similarity 28.8%; Pred. No. 3.8e-09;
Matches 51; Conservative 30; Mismatches 78; Indels 18; Gaps 5;

QY 41 GGQVRQRYLYTDDAQOEAHLEIREDTGTVGGAADQSPESLLQALKKPGVIOILGVKTSR 100
Db 40 GGAPRRKLYC-----ATKYHLQHPGSRVNGSLNSAYSILLETAVGVVAIKLFSGR 95
QY 101 FLCQPDGALYGLHFDPEACSFRELLLEDGYNVYQSEAHGLPLHLPGNKSP--HRDPAP 158
Db 96 YLAMNKRGLYASDHYNAE-CEVERIHGELGYNTYASR-----LYRTGSSGPGAQRPQGA 149
QY 159 RGP-----ARFLPLGLPPAPPEPGIILAPQPPDVGSSDPLSMVGPQSGRSPSYAS 209
Db 150 QRPWTVSVNGKGRPRGRFTRTKQSSLFPLRVLGHKDHEMWRLQLQSSQPRAPGEGS 206

RESULT 3

US-08-438-439C-7
; Sequence 7, Application US/08438439C
; Patent No. 5876967
; GENERAL INFORMATION:
; APPLICANT: Nathans, Jeremy
; APPLICANT: Smallwood, Phillip M.
; APPLICANT: Macke, Jennifer P.
; TITLE OF INVENTION: FIBROBLAST GROWTH FACTOR HOMOLOGOUS
; TITLE OF INVENTION: FACTOR-2 AND METHODS OF USE
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/438,439C
; FILING DATE: May 12, 1995
; CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
; NAME: Haile, Lisa A.
; REGISTRATION NUMBER: 38,347
; REFERENCE/DOCKET NUMBER: 07265/046001

TELEPHONE: 619/678-5070
; TELECOMMUNICATION INFORMATION:
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 245 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-438-439C-7

Query Match 16.0%; Score 179; DB 2; Length 245;
Best Local Similarity 28.8%; Pred. No. 3.8e-09;
Matches 51; Conservative 30; Mismatches 78; Indels 18; Gaps 5;

QY 41 GGQVRQRYLYTDDAQOEAHLEIREDTGTVGGAADQSPESLLQALKKPGVIOILGVKTSR 100
Db 40 GGAPRRKLYC-----ATKYHLQHPGSRVNGSLNSAYSILLETAVGVVAIKLFSGR 95
QY 101 FLCQPDGALYGLHFDPEACSFRELLLEDGYNVYQSEAHGLPLHLPGNKSP--HRDPAP 158
Db 96 YLAMNKRGLYASDHYNAE-CEVERIHGELGYNTYASR-----LYRTGSSGPGAQRPQGA 149
QY 159 RGP-----ARFLPLGLPPAPPEPGIILAPQPPDVGSSDPLSMVGPQSGRSPSYAS 209
Db 150 QRPWTVSVNGKGRPRGRFTRTKQSSLFPLRVLGHKDHEMWRLQLQSSQPRAPGEGS 206

RESULT 4

US-08-439-725A-14
; Sequence 14, Application US/08439725A
; Patent No. 5693775
; GENERAL INFORMATION:
; APPLICANT: Nathans, Jeremy
; APPLICANT: Smallwood, Philip M.
; APPLICANT: Macke, Jennifer P.
; TITLE OF INVENTION: FIBROBLAST GROWTH FACTOR HOMOLOGOUS
; TITLE OF INVENTION: FACTOR-1 (FHF-1) AND METHODS OF USE

```
;/ NUMBER OF SEQUENCES: 15
;/ CORRESPONDENCE ADDRESS:
;/ ADDRESSEE: Fish & Richardson P.C.
;/ STREET: 4225 Executive Square, Suite 1400
;/ CITY: La Jolla
;/ STATE: CA
;/ COUNTRY: USA
;/ ZIP: 92037
;/ COMPUTER READABLE FORM:
;/ MEDIUM TYPE: Floppy disk
;/ COMPUTER: IBM PC compatible
;/ OPERATING SYSTEM: PC-DOS/MS-DOS
;/ SOFTWARE: PatentIn Release #1.0, Version #1.30
;/ CURRENT APPLICATION DATA:
;/ APPLICATION NUMBER: US/08/439,725A
;/ FILING DATE: 12-MAY-1995
;/ CLASSIFICATION: 424
;/ ATTORNEY/AGENT INFORMATION:
;/ NAME: Haile, Lisa A.
;/ REGISTRATION NUMBER: 38,347
;/ REFERENCE/DOCKET NUMBER: 07265/047001
;/ TELECOMMUNICATION INFORMATION:
;/ TELEPHONE: 619/678-5099
;/ TELEFAX: 617/678-5099
;/ INFORMATION FOR SEQ ID NO: 14:
;/ SEQUENCE CHARACTERISTICS:
;/ LENGTH: 198 amino acids
;/ TYPE: amino acid
;/ STRANDEDNESS: not relevant
;/ TOPOLOGY: linear
;/ MOLECULE TYPE: protein
;/ US-08-439-725A-14

Query Match 15.8%; Score 176.5; DB 1; Length 198;
Best Local Similarity 29.1%; Pred. No. 4.9e-09;
Matches 46; Conservative 27; Mismatches 52; Indels 33; Gaps 6;

QY 13 LWSVVLGALLGACQHP-----IPDS---SPLLQ-----FGQV----- 44
Db 12 LWALVFLGILVGMVVPSPAGTRANNTLLDSRGWGTLLSRAGLAGTAGVNWESGYLVG 71
QY 45 --RQRLYTDQAQTEAHLEIREDTGVTGGADQSPESLLQKALPGVQIQLGVKTSRFL 102
Db 72 IKRRLYCNVG--IGFHLQVLPDRISGTHEENPYSLLEISTVERGVVSLFGVRSALFV 129
QY 103 CORPDGALYGLSHFDPEACSFRELLEDGYNVYQSEAH 140
Db 130 AMNSKGRLYATPSFQ-BECKFRETLLPNNYNAYESDLY 166

RESULT 5
US-08-441-629-12
; Sequence 12, Application US/08441629
; Patent No. 5766923
; GENERAL INFORMATION:
; APPLICANT: Kirschner, Marc W.
; APPLICANT: Kinoshita, No. 5766923iyuki
; TITLE OF INVENTION: RECEPTOR-LIGAND ASSAY
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
```

```
;/ APPLICATION NUMBER: US/08/441,629
;/ FILING DATE: 15-MAY-1995
;/ CLASSIFICATION: 435
;/ PRIOR APPLICATION DATA:
;/ APPLICATION NUMBER: US 08/279,217
;/ FILING DATE: 22-JUL-1994
;/ ATTORNEY/AGENT INFORMATION:
;/ NAME: Granahan, Patricia
;/ REGISTRATION NUMBER: 32,227
;/ REFERENCE/DOCKET NUMBER: H095-01A
;/ TELECOMMUNICATION INFORMATION:
;/ TELEPHONE: (617) 861-6240
;/ TELEFAX: (617) 861-9540
;/ INFORMATION FOR SEQ ID NO: 12:
;/ SEQUENCE CHARACTERISTICS:
;/ LENGTH: 198 amino acids
;/ TYPE: amino acid
;/ STRANDEDNESS: single
;/ TOPOLOGY: linear
;/ MOLECULE TYPE: protein
;/ US-08-441-629-12

Query Match 15.8%; Score 176.5; DB 1; Length 198;
Best Local Similarity 29.1%; Pred. No. 4.9e-09;
Matches 46; Conservative 27; Mismatches 52; Indels 33; Gaps 6;

QY 13 LWSVVLGALLGACQHP-----IPDS---SPLLQ-----FGQV----- 44
Db 12 LWALVFLGILVGMVVPSPAGTRANNTLLDSRGWGTLLSRAGLAGTAGVNWESGYLVG 71
QY 45 --RQRLYTDQAQTEAHLEIREDTGVTGGADQSPESLLQKALPGVQIQLGVKTSRFL 102
Db 72 IKRRLYCNVG--IGFHLQVLPDRISGTHEENPYSLLEISTVERGVVSLFGVRSALFV 129
QY 103 CORPDGALYGLSHFDPEACSFRELLEDGYNVYQSEAH 140
Db 130 AMNSKGRLYATPSFQ-BECKFRETLLPNNYNAYESDLY 166

RESULT 6
US-08-867-471-14
; Sequence 14, Application US/08867471
; Patent No. 5872226
; GENERAL INFORMATION:
; APPLICANT: Nathans, Jeremy
; APPLICANT: Smallwood, Philip M.
; APPLICANT: Macke, Jennifer P.
; TITLE OF INVENTION: FIBROBLAST GROWTH FACTOR HOMOLOGOUS
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/867,471
; FILING DATE: 02-JUN-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/439,725
; FILING DATE: 12-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Haile, Lisa A.
; REGISTRATION NUMBER: 38,347
```

REFERENCE/DOCKET NUMBER: 07265/047001
TELECOMMUNICATION INFORMATION:

TELEPHONE: 619/678-5070

TELEFAX: 619/678-5099

INFORMATION FOR SEQ ID NO: 14:

SEQUENCE CHARACTERISTICS:

LENGTH: 198 amino acids

TYPE: amino acid

STRANDEDNESS: not relevant

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-867-471-14

Query Match 15.8%; Score 176.5; DB 2; Length 198;

Best Local Similarity 29.1%; Pred. No. 4.9e-09;

Matches 46; Conservative 27; Mismatches 52; Indels 33; Gaps 6;

QY 13 LWSVLAGLLGACQAH-----IPDS---SPLIQ-----FGQV----- 44

DB 12 LWALVFLGILVGMVPSAGTRANNLLDSRGWGTLLSRAGLAGEIAGVNWESGYLVG 71

QY 45 --RORYLYTDDAQOQTEAHLEIREDTGVTGGAAQSPESLLQLKALKPGVIQILGVKTSRFL 102

DB 72 IKRQRLRYCNGV--IGFHLQVLPDGRISGTHEENPYSLLLEISTVERGVVSLFGVRSALFV 129

QY 103 CORPDGALYGLHFDPEACSFRELLEDGYNVYQSEAH 140

DB 130 AMNSKGRLYATPSFQ-ECKFRETLLPNNYNAYESDLY 166

RESULT 7

US-08-438-439C-10

Sequence 10, Application US/08438439C

Patent No. 5876967

GENERAL INFORMATION:

APPLICANT: Nathans, Jeremy

APPLICANT: Smallwood, Phillip M.

APPLICANT: Macke, Jennifer P.

TITLE OF INVENTION: FIBROBLAST GROWTH FACTOR HOMOLOGOUS

NUMBER OF INVENTION: FACTOR-2 AND METHODS OF USE

NUMBER OF SEQUENCES: 25

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Richardson P.C.

STREET: 4225 Executive Square, Suite 1400

CITY: La Jolla

STATE: CA

COUNTRY: USA

ZIP: 92037

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/438,439C

FILING DATE: May 12, 1995

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Haile, Lisa A.

REGISTRATION NUMBER: 38,347

REFERENCE/DOCKET NUMBER: 07265/046001

TELEPHONE: 619/678-5070

TELEFAX: 619/678-5099

INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:

LENGTH: 198 amino acids

TYPE: amino acid

STRANDEDNESS: not relevant

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-438-439C-10

Query Match 15.8%; Score 176.5; DB 2; Length 198;

Best Local Similarity 29.1%; Pred. No. 4.9e-09;

Matches 46; Conservative 27; Mismatches 52; Indels 33; Gaps 6;

QY 13 LWSVLAGLLGACQAH-----IPDS---SPLIQ-----FGQV----- 44

DB 12 LWALVFLGILVGMVPSAGTRANNLLDSRGWGTLLSRAGLAGEIAGVNWESGYLVG 71

QY 45 --RORYLYTDDAQOQTEAHLEIREDTGVTGGAAQSPESLLQLKALKPGVIQILGVKTSRFL 102

DB 72 IKRQRLRYCNGV--IGFHLQVLPDGRISGTHEENPYSLLLEISTVERGVVSLFGVRSALFV 129

QY 103 CORPDGALYGLHFDPEACSFRELLEDGYNVYQSEAH 140

DB 130 AMNSKGRLYATPSFQ-ECKFRETLLPNNYNAYESDLY 166

RESULT 8

US-08-438-439C-20

Sequence 20, Application US/08438439C

Patent No. 5876967

GENERAL INFORMATION:

APPLICANT: Nathans, Jeremy

APPLICANT: Smallwood, Phillip M.

APPLICANT: Macke, Jennifer P.

TITLE OF INVENTION: FIBROBLAST GROWTH FACTOR HOMOLOGOUS

NUMBER OF INVENTION: FACTOR-2 AND METHODS OF USE

NUMBER OF SEQUENCES: 25

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Richardson P.C.

STREET: 4225 Executive Square, Suite 1400

CITY: La Jolla

STATE: CA

COUNTRY: USA

ZIP: 92037

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/438,439C

FILING DATE: May 12, 1995

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Haile, Lisa A.

REGISTRATION NUMBER: 38,347

REFERENCE/DOCKET NUMBER: 07265/046001

TELEPHONE: 619/678-5070

TELEFAX: 619/678-5099

INFORMATION FOR SEQ ID NO: 20:

SEQUENCE CHARACTERISTICS:

LENGTH: 198 amino acids

TYPE: amino acid

STRANDEDNESS: not relevant

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-438-439C-20

Query Match 15.8%; Score 176.5; DB 2; Length 198;

Best Local Similarity 29.1%; Pred. No. 4.9e-09;

Matches 46; Conservative 27; Mismatches 52; Indels 33; Gaps 6;

QY 13 LWSVLAGLLGACQAH-----IPDS---SPLIQ-----FGQV----- 44

DB 12 LWALVFLGILVGMVPSAGTRANNLLDSRGWGTLLSRAGLAGEIAGVNWESGYLVG 71

QY 45 --RORYLYTDDAQOQTEAHLEIREDTGVTGGAAQSPESLLQLKALKPGVIQILGVKTSRFL 102

DB 72 IKRQRLRYCNGV--IGFHLQVLPDGRISGTHEENPYSLLLEISTVERGVVSLFGVRSALFV 129


```

: NAME: NEUNER, George W
: REGISTRATION NUMBER: 26964
: REFERENCE/POCKET NUMBER: 44146
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (617)523-3400
: TELEFAX: (617)523-6440
: TELEX: 200291 STRE UR
: INFORMATION FOR SEQ ID NO: 5:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 207 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-08-902-233-5

```

Query Match 15.8%; Score 176.5; DB 3; Length 207;
Best Local Similarity 29.1%; Pred. No. 5.2e-09;
Matches 46; Conservative 27; Mismatches 52; Indels 33; Gaps 6;

21 LMAVLTGTLGLGVWVPSPAGTKRANNTLLDUSKMGWLLLSRSKRALAGEIAGVNWSGGVLNG 80
QY 45 --RORYLTDDAQOATEAHLEIRETDVGGAADOSPESLILKALKPGVIQTLYGSKRFL 102
Db 81 IKQRRLVCNVG--IGFHLQVLDPGRISTGHENPYSILLEITSVBERGVVSFLFGVRSALFV 138
QY 103 CQRPDGALYGSILHFDPEACSFRELLLEDGYNVYOSEAH 140

DD	QY	103	CQRPDGALYGSLIHPDPEACSFRELLLEDGYNVYQSEAH	140
DD			: : :	
DD	Db	139	AMNSGRILVYPSQO-EECAFRFETLLPNNNVAYESDLY	175
DD			: : :	
DD	81	IRKQRKLYCNVG--IGFHLQVLPDGRLSGTHEENPYLSLELTSTVERGVVSLFGVRSALFV	13	

DB 139 AMNSKGRDIATPSFQ-EECAFREIILFFNNINAYESDLY 1/3

US-08-531-1/1-b
; Sequence 6, Application US/08551171
; Patent No. 5679550
; GENERAL INFORMATION:
; APPLICANT: YOSHIMURA, Koji
; APPLICANT: ISHIMARU, Kaori

APPLICANT: ISHIMARU, KOICHI
 APPLICANT: IGARASHI, KOICHI
 APPLICANT: TERADA, Masaaki
 TITLE OF INVENTION: hst-2 MUTEN, DNA CODING FOR THE SAME AND PREPARATION THEREOF
 TITLE OF INVENTION: hst-2 MUTEN, DNA CODING FOR THE SAME AND PREPARATION THEREOF
 NUMBER OF SEQUENCES: 10
 CORRESPONDENCE ADDRESS:

TITLE OF INVENTION: PREPARATION THEREOF
 NUMBER OF SEQUENCES: 10
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &
 ADDRESSEE: CUSHMAN
 STREET: 130 Water Street
 CITY: Boston
 STATE: Massachusetts
 COUNTRY: US
 ZIP: 02109

```

/ ZIP: 02109
/
/ COMPUTER READABLE FORM:
/
/ MEDIUM TYPE: Floppy disk
/
/ COMPUTER: IBM PC compatible
/
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/
/ CURRENT APPLICATION DATA:
/
/ APPLICATION NUMBER: US/08/551,171
/
/ FILING DATE:
/

```

APPLICATION NUMBER: US/08/351,171
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/196,001
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: NEUNER, George W
REGISTRATION NUMBER: 26964
REFERENCE/DOCKET NUMBER: 44146

REFERENCE/DOCKET NUMBER: 44146
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)523-3400
TELEFAX: (617)523-6440
TELEX: 200291 STRE UR

; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 208 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-551-171-6

Query Match 15.8%; Score 176.5; DB 1; Length 208;
Best Local Similarity 29.1%; Pred. No. 5.2e-09;
Matches 46; Conservative 27; Mismatches 52; Indels 33; Gaps 6;
QY 13 LWSVLAGLLGACQHP-----IPDS---SPLLQ-----FGQV----- 44
Db 22 LWALVFLGLVGMVPSAGTRANTLLDSRGWGTLLSRAGLAGETAGVNWESGYLVG 81
QY 45 --RQRYLYTDDAQTEAHLEIREDTGVGGAQDQSPESLIQLKALKPGVIOILGVKTSRFL 102
Db 82 IKRRLRYCNVG--IGFHLQVLPDGRISGTHEENPYSLLEISTVERGVVSLFGVRSALFV 139
QY 103 CORPDGALYGSLEHDPACSFRELLEDGYNVYQSEAH 140
Db 140 AMNSKRLYATPSFQ-EECKFRETLPPNNYAYESDLY 176

Search completed: August 6, 2001, 21:05:42
Job time: 1063 sec

Result No.	Query Match	Score	Length	DB	ID	Description
1	803.5	72.0	210	21	AAB18636	Amino acid sequenc
2	780	69.9	153	22	AAB73069	Human fibroblast g
3	273	24.5	214	20	AAV08581	Human PRO533 prote
4	273	24.5	216	20	AAV08583	Human PRO533 prote
5	273	24.5	216	20	AAV13353	Amino acid sequenc
6	273	24.5	216	20	AAV05280	FGF-8 homologue pr
7	273	24.5	216	21	AAB33434	Human PRO533 prote
8	273	24.5	216	21	AAV88568	Human PRO533 amino
9	273	24.5	216	22	AAB68593	PRO533. Homo sapi
10	273	24.5	216	22	AAB31201	Amino acid sequenc
11	273	24.5	216	22	AAB80221	Human PRO533 prote

ALIGNMENTS

RESULT 1

AAB18636
ID AAB18636 standard; Protein; 210 AA.

AC AAB18636;

DT 22-JAN-2001 (first entry)

DE Amino acid sequence of murine fibroblast growth factor (FGF)-21.

pd10-VEGFuc; gene delivery vector; eye disease; neovascular disease;
 neurotrophic factor; anti-angiogenic factor; eye disease; glaucoma;
 macular degeneration; diabetic retinopathy; retinitis pigmentosa;
 inherited retinal degeneration; surgery-induced retinopathy;
 retinal detachment; photic retinopathy; toxic retinopathy;
 trauma-induced retinopathy; wet age related macular degeneration;
 ARMD; retinopathy; fibroblast growth factor-20; FGF-20

Mus sp.

PN WO200054813-A2.

PD 21-SEP-2000.

PF 15-MAR-2000; 2000WO-US07062.

PR 15-MAR-1999; 99US-0124460.

[illegible]

PA (CHIC) CITRON CONF.
(REGC) UNIV CALIFORNIA.

PI Manning WC, Dwarki VJ,

TO : SAC, NEW YORK
FROM : SAC, ALBANY
SUBJECT: [REDACTED]
[REDACTED]

XX WPI; 1999-347718/29.
 XX Nucleic acid encoding fibroblast growth factor - 19, useful for the
 PT diagnosis, prevention and treatment of cancers
 PT
 XX Disclosure; Fig 3; 88pp; English.
 XX This invention describes a novel human fibroblast growth factor, PRO533,
 CC also known as fibroblast growth factor-19 (FGF-19). The nucleic acids,
 CC methods and PRO533 polypeptides disclosed may be used in the diagnosis
 CC and treatment of tumours and/or conditions characterized by modulation of
 CC PRO533 expression, or in the preparation of compositions for such
 CC therapies. These compositions and methods may be used in the diagnosis
 CC and treatment of neoplastic cell growth and proliferation in mammals
 CC (especially humans). The invention is based on the identification of
 CC genes that are amplified in the genome of tumour cells. Such gene
 CC amplification is expected to be associated with the over expression of
 CC the gene product and contribute to tumourgenesis and/or autocrine
 CC signalling. Accordingly, the proteins encoded by the amplified genes are
 CC believed to be useful targets for the diagnosis and/or treatment of
 CC certain cancers and may act as predictors of the prognosis for tumour
 CC treatments.
 XX Sequence 214 AA;
 SQ

Query Match 24.5%; Score 273; DB 20; Length 214;
 Best Local Similarity 36.8%; Pred. No. 3.5e-16;
 Matches 78; Conservative 27; Mismatches 81; Indels 26; Gaps 9;

QY 11 SGLWVSLAGLLGACQAHPIPDSSPLLOF--GGQVRQRYLYTDDAQ-QTEAHLIEIREDG 67
 Db 12 aglwlav-agrpia-----fsdagphvhygwdpirlrlhlytsgphglsscfliradg 64
 QY 68 TVGGAADQSPESLLQALKPKGVITLGVKTSRFLCQRPDGLYGLSHLHFDPEACSFRELL 127
 Db 65 vdcargqgahsllleikavaltvaikgvhsrvlycmgagdkmqgllqgyseedcafeeei 124
 QY 128 LEDGYNVYQSEAHGLPLHLPGNKSHPRDPAAPRGPARFLP----LPGLPPAPPEPPI--- 180
 Db 125 rpdgynvyrsekhrpvsissakq-rqlyknrg---flplshfplmpmvppeedlgrh 180
 QY 181 ----LAPQPPDVGSSDPLSMV-GPSQGRSPSY 207
 Db 181 lesdmfsspletmdmpfglvtgleavrpspsf 212

RESULT 4
 AAY08583
 ID AAY08583 standard; Protein; 216 AA.
 XX AAY08583;
 AC
 XX 05-AUG-1999 (first entry)
 DT
 XX Human PRO533 protein fragment.
 DE
 XX PRO533; FGF-19; fibroblast growth factor; human; diagnosis; treatment;
 KW tumour; neoplastic cell growth; cell proliferation; tumourgenesis; cancer;
 KW autocrine signalling.
 XX
 OS Homo sapiens.
 XX
 PN WO9927100-A1.
 XX
 XX 03-JUN-1999.
 PD
 XX 25-NOV-1998; 98WO-US25190.
 PF
 XX 21-SEP-1998; 98US-0158432.
 PR
 XX 25-NOV-1997; 97US-0066840.
 XX

PA (GETH) GENENTECH INC.
 XX Botstein D, Goddard A, Gurney AL, Hillan KJ, Lawrence DA;
 PI Roy MA;
 XX WPI; 1999-347718/29.
 DR
 XX Nucleic acid encoding fibroblast growth factor - 19, useful for the
 PT diagnosis, prevention and treatment of cancers
 PT
 XX Disclosure; Fig 11; 88pp; English.
 PS
 XX This invention describes a novel human fibroblast growth factor, PRO533,
 CC also known as fibroblast growth factor-19 (FGF-19). The nucleic acids,
 CC methods and PRO533 polypeptides disclosed may be used in the diagnosis
 CC and treatment of tumours and/or conditions characterized by modulation of
 CC PRO533 expression, or in the preparation of compositions for such
 CC therapies. These compositions and methods may be used in the diagnosis
 CC and treatment of neoplastic cell growth and proliferation in mammals
 CC (especially humans). The invention is based on the identification of
 CC genes that are amplified in the genome of tumour cells. Such gene
 CC amplification is expected to be associated with the over expression of
 CC the gene product and contribute to tumourgenesis and/or autocrine
 CC signalling. Accordingly, the proteins encoded by the amplified genes are
 CC believed to be useful targets for the diagnosis and/or treatment of
 CC certain cancers and may act as predictors of the prognosis for tumour
 CC treatments.
 XX Sequence 216 AA;
 SQ

Query Match 24.5%; Score 273; DB 20; Length 216;
 Best Local Similarity 36.8%; Pred. No. 3.6e-16;
 Matches 78; Conservative 27; Mismatches 81; Indels 26; Gaps 9;

QY 11 SGLWVSLAGLLGACQAHPIPDSSPLLOF--GGQVRQRYLYTDDAQ-QTEAHLIEIREDG 67
 Db 14 aglwlav-agrpia-----fsdagphvhygwdpirlrlhlytsgphglsscfliradg 66
 QY 68 TVGGAADQSPESLLQALKPKGVITLGVKTSRFLCQRPDGLYGLSHLHFDPEACSFRELL 127
 Db 67 vdcargqgahsllleikavaltvaikgvhsrvlycmgagdkmqgllqgyseedcafeeei 126
 QY 128 LEDGYNVYQSEAHGLPLHLPGNKSHPRDPAAPRGPARFLP----LPGLPPAPPEPPI--- 180
 Db 127 rpdgynvyrsekhrpvsissakq-rqlyknrg---flplshfplmpmvppeedlgrh 182
 QY 181 ----LAPQPPDVGSSDPLSMV-GPSQGRSPSY 207
 Db 183 lesdmfsspletmdmpfglvtgleavrpspsf 214

RESULT 5
 AAY13353
 ID AAY13353 standard; Protein; 216 AA.
 XX AAY13353;
 AC
 XX 25-JUN-1999 (first entry)
 DT
 XX Amino acid sequence of protein PRO533.
 DE
 XX Secreted protein; transmembrane protein; human; enterocolitis;
 KW Zollinger-Ellison syndrome; gastrointestinal ulceration;
 KW congenital microvillus atrophy; skin disease; cell growth;
 KW abnormal keratinocyte differentiation; psoriasis; epithelial cancer;
 KW Parkinson's disease; Alzheimer's disease; ALS; neuropathy;
 KW fibromodulin; dermal scarring; Usher Syndrome; Atrophia areata;
 KW anti-thrombotic; wound healing; tissue repair.
 XX
 OS Homo sapiens.
 XX
 PN WO9914328-A2.

XX PD 25-MAR-1999.
 XX PF 16-SEP-1998; 98WO-US19330.
 XX PR 25-NOV-1997; 97US-0066840.
 PR 17-SEP-1997; 97US-0059113.
 PR 17-SEP-1997; 97US-0059115.
 PR 17-SEP-1997; 97US-0059117.
 PR 17-SEP-1997; 97US-0059119.
 PR 17-SEP-1997; 97US-0059121.
 PR 17-SEP-1997; 97US-0059122.
 PR 17-SEP-1997; 97US-0059124.
 PR 18-SEP-1997; 97US-0059263.
 PR 18-SEP-1997; 97US-0059266.
 PR 15-OCT-1997; 97US-0082125.
 PR 17-OCT-1997; 97US-0062285.
 PR 17-OCT-1997; 97US-0062287.
 PR 21-OCT-1997; 97US-0063486.
 PR 24-OCT-1997; 97US-0062814.
 PR 24-OCT-1997; 97US-0063045.
 PR 24-OCT-1997; 97US-0063120.
 PR 24-OCT-1997; 97US-0063121.
 PR 24-OCT-1997; 97US-0063127.
 PR 24-OCT-1997; 97US-0063128.
 PR 27-OCT-1997; 97US-0063329.
 PR 27-OCT-1997; 97US-0063327.
 PR 28-OCT-1997; 97US-0063341.
 PR 28-OCT-1997; 97US-0063542.
 PR 28-OCT-1997; 97US-0063544.
 PR 28-OCT-1997; 97US-0063549.
 PR 28-OCT-1997; 97US-0063550.
 PR 28-OCT-1997; 97US-0063564.
 PR 29-OCT-1997; 97US-0063435.
 PR 29-OCT-1997; 97US-0063704.
 PR 29-OCT-1997; 97US-0063732.
 PR 29-OCT-1997; 97US-0063738.
 PR 29-OCT-1997; 97US-0063734.
 PR 29-OCT-1997; 97US-0084215.
 PR 29-OCT-1997; 97US-0083735.
 PR 31-OCT-1997; 97US-0063870.
 PR 31-OCT-1997; 97US-0064103.
 PR 03-NOV-1997; 97US-0064248.
 PR 07-NOV-1997; 97US-0064809.
 PR 12-NOV-1997; 97US-0065196.
 PR 17-NOV-1997; 97US-0065846.
 PR 18-NOV-1997; 97US-0065693.
 PR 21-NOV-1997; 97US-0066120.
 PR 21-NOV-1997; 97US-0066120.
 PR 24-NOV-1997; 97US-0066772.
 PR 24-NOV-1997; 97US-0066466.
 PR 24-NOV-1997; 97US-0066770.
 PR 24-NOV-1997; 97US-0066511.
 PR 24-NOV-1997; 97US-0066453.
 XX PA (GETH) GENENTECH INC.
 XX PI Chen J, Goddard A, Gurney AL, Pennica D, Wood WI, Yuan J;
 XX DR WPI; 1999-229533/19.
 DR N-PSDB; AAX52224.
 XX PT New isolated human genes and polypeptides used in, e.g. treatment of
 PT gastrointestinal ulceration
 XX PS Claim 12; Fig 22; 320pp; English.
 XX CC AAV13344-403 represent secreted and transmembrane human proteins.
 CC The cDNA sequences are obtained from cDNA libraries, prepared from
 CC fetal lung, fetal kidney, fetal brain, fetal liver and fetal retina.
 CC The encoded polypeptides have specific uses based on their homology to
 CC known polypeptides, e.g. PRO211 and PRO217 can be used for disorders

CC associated with the preservation and maintenance of gastrointestinal
 CC mucosa and the repair of acute and chronic mucosal lesions
 CC (e.g. enterocolitis, Zollinger-Ellison syndrome, gastrointestinal
 CC ulceration and congenital microvillus atrophy), skin diseases associated
 CC with abnormal keratinocyte differentiation (e.g. psoriasis, epithelial
 CC cancers such as lung squamous cell carcinoma of the vulva and gliomas),
 CC potent effects on cell growth and development, diseases related to
 CC growth or survival of nerve cells including Parkinson's disease,
 CC Alzheimer's disease, ALS, neuropathies or cancer. PRO265 can be used as
 CC for fibromodulin, e.g. for reducing dermal scarring. PRO264 can be used
 CC as a target for anti-tumor drugs. PRO533 may be used in the treatment
 CC of Usher Syndrome or Atrophia areata; PRO269 can be used as an
 CC anti-thrombotic agent; PRO287 polypeptides and portions may have
 CC therapeutic applications in wound healing and tissue repair; PRO317 can
 CC be used for treating problems of the kidney, uterus, endometrium, blood
 CC vessels, or related tissue, e.g. in the heart of genital tract.
 XX SQ Sequence 216 AA;
 Query Match 24.5%; Score 273; DB 20; Length 216;
 Best Local Similarity 36.8%; Pred. No. 3.6e-16;
 Matches 78; Conservative 27; Mismatches 81; Indels 26; Gaps 9;
 QY 11 SGLWVSVLGALLGACQAHPIPDSPSLQF--GGQVRQRYLYTDDAQ-QTEAHLREDDG 67
 Db 14 aglwav-agrpla-----fsdagphvhygwgdpirlrhlytsgphglsccflriradg 66
 QY 68 TVGGAADQSPESLLQLKALKPGVQILGVKTSRFLCORPDGALYGLHFDPEACSPRELL 127
 Db 67 vvdcarqgsahsilleikavalrtvaikgvhsrvylcmgadgkmgqllgyseedcafeesi 126
 QY 128 LEDGVNYVOSEAHGLPLHLPGNKSPhRDPAKGRFELP----LPGLPPAPPEPGI--- 180
 Db 127 rpdgynvrsekhrfpvsissakq-rqlyknrg---flplshflpmipmvpeepdirgh 182
 QY 181 ----LAPQPPDVGSSDPLSNV-GPSQGRSPSY 207
 Db 183 lesdmfsspletmdmpfglvtgleavirpsf 214
 AC AAY05280;
 XX 22-JUN-1999 (first entry)
 DE FGF-8 homologue PRO533.
 KW Antibody; PRO187; PRO533; PRO214; PRO240; PRO211; PRO230; PRO261; PRO246;
 KW EBAF-2; inhibitor; tumour growth; cancer; EGF-like homologue;
 KW FGF-8 homologue.
 XX OS Homo sapiens.
 XX PN WO9914327-A2.
 XX PD 25-MAR-1999.
 XX PF 10-SEP-1998; 98WO-US18824.
 XX PR 25-NOV-1997; 97US-0066840.
 PR 17-SEP-1997; 97US-0059114.
 PR 17-SEP-1997; 97US-0059117.
 PR 18-SEP-1997; 97US-0059263.
 PR 15-OCT-1997; 97US-0062125.
 PR 17-OCT-1997; 97US-0062285.
 PR 17-OCT-1997; 97US-0062287.
 PR 24-OCT-1997; 97US-0062816.
 PR 29-OCT-1997; 97US-0063704.
 XX

Db 169 intpiprrhrsaeddsrdplnvklprarmtpapas 205

RESULT 15
AYY08582
ID AYY08582 standard; Protein; 213 AA.
XX
AC AAY08582;
XX
DT 05-AUG-1999 (first entry)
XX
DE Human FGF-15 protein fragment.
XX
KW PRO533; FGF-19; fibroblast growth factor; human; diagnosis; treatment;
tumor; neoplastic cell growth; cell proliferation; tumorigenesis; cancer;
autocrine signalling; FGF-15.

OS Homo sapiens.
XX
PN WO9927100-Al.
XX
PD 03-JUN-1999.
XX
PE 25-NOV-1998; 98WO-US25190.
XX
PR 21-SEP-1998; 98US-0158432.
PR 25-NOV-1997; 97US-0068840.
XX
PA (GETH.) GENENTECH INC.
XX
PI Rotstein D, Goddard A, Gurney AL, Hillan KJ, Lawrence DA;
Roy MA;
DR WPI; 1999-347718/29.
XX
PT Nucleic acid encoding fibroblast growth factor - 19, useful for the
diagnosis, prevention and treatment of cancers
PT Disclosure; Fig 3; 88pp; English.
PS This invention describes a novel human fibroblast growth factor, PRO533,
also known as fibroblast growth factor-19 (FGF-19). The nucleic acids,
methods and PRO533 polypeptides disclosed may be used in the diagnosis
and treatment of tumors and/or conditions characterized by modulation of
PRO533 expression, or in the preparation of compositions for such
therapies. These compositions and methods may be used in the diagnosis
and treatment of neoplastic cell growth and proliferation in mammals
(especially humans). The invention is based on the identification of
genes that are amplified in the genome of tumor cells. Such gene
amplification is expected to be associated with the over expression of
the gene product and contribute to tumorigenesis and/or autocrine
signalling. Accordingly, the proteins encoded by the amplified genes are
believed to be useful targets for the diagnosis and/or treatment of
certain cancers and may act as predictors of the prognosis for tumor
treatments.

XX SQ Sequence 213 AA;

Query Match 18.5%; Score 206.5; DB 20; Length 213;
Best Local Similarity 33.8%; Pred. No. 2e-10;
Matches 53; Conservative 29; Mismatches 70; Indels 5; Gaps 4

Qy 13 LWSVLGLAGLLGCQAHPDPSSPLLOFG-GGV-RQRILYTDDAQQTAEHLEIREDTVG 70
||| : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Dl lwlavsrpl--adqsqvsdedplfygwktrlylsagpyvsnclfrsrgsdv 71
||| : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Qy 71 GAADQSPESLIOLKALPGVTIOILGVKTSTRFLCQRPDGALXGSLHFDEPACSFRLELLE 130
||| : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Dl 72 ceedqnrllefrvalktaikdvsvrlycmsadgkiylirseedctfreemdl 131
||| : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Qy 131 GYNVYOSEAHGLPHLPNGNKSPPHRDPAPRGARFLPL 167
||| : | : | : | : | : | : | : | : | : | : | : | : | : | : | :

Db 132 gyoqysmkhhlhifiqak-preslqddkpsnfipv 167

Search completed: August 6, 2001, 20:57:48
Job time: 9720 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 6, 2001, 21:43:02 ; Search time 1964.36 Seconds
(without alignments)
3123.105 Million cell updates/sec

Title: US-09-391-861-3
Perfect score: 649
Sequence: 1 atggaatgatgatgatctag.....ctgacttttctgaaatcta 649

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 10228115 seqs, 4726426750 residues 20456230
Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
4: gb_est4:*
5: gb_est5:*
6: gb_est6:*
7: gb_est7:*
8: gb_est8:*
9: gb_est9:*
10: gb_est10:*
11: gb_est11:*
12: gb_est12:*
13: gb_est13:*
14: gb_est14:*
15: gb_est15:*
16: gb_est16:*
17: gb_est17:*
18: gb_est18:*
19: gb_est19:*
20: gb_est20:*
21: gb_est21:*
22: gb_est22:*
23: gb_est23:*
24: gb_est24:*
25: gb_est33:*
26: gb_est34:*
27: gb_est35:*
28: gb_est36:*
29: gb_est37:*
30: gb_est38:*
31: gb_est39:*
32: gb_est40:*
33: em_estba:*
34: em_estfun:*
35: em_esthum1:*
36: em_esthum2:*
37: em_esthum3:*
38: em_esthum4:*
39: em_esthum5:*
40: em_esthum6:*
41: em_esthum7:*
42: em_esthum8:*
43: em_esthum9:*
44: em_esthum10:*
45: em_esthum11:*
46: em_esthum12:*
47: em_esthum13:*
48: em_esthum14:*
49: em_esthum15:*
50: em_esthum16:*
51: em_esthum17:*
52: em_esthum18:*
53: em_esthum19:*
54: em_esthum20:*
55: em_esthum21:*
56: em_esthum22:*
57: em_esthum23:*
58: em_esthum24:*
59: em_esthum25:*
60: em_esthum26:*
61: em_esthum27:*
62: em_esthum28:*
63: em_estin1:*
64: em_estin2:*
65: em_estin3:*
66: em_estin4:*
67: em_estin5:*
68: em_estomi:*
69: em_estom2:*
70: em_estov1:*
71: em_estov2:*
72: em_estpl1:*
73: em_estpl2:*
74: em_estpl3:*
75: em_estpl4:*
76: em_estpl5:*
77: em_estpl6:*
78: em_estpl7:*
79: em_estpl8:*
80: em_estpl9:*
81: em_estpl10:*
82: em_estro1:*
83: em_estro2:*
84: em_estro3:*
85: em_estro4:*
86: em_estro5:*
87: em_estro6:*
88: em_estro7:*
89: em_estro8:*
90: em_estro9:*
91: em_estro10:*
92: em_estro11:*
93: em_estro12:*
94: em_estro13:*
95: em_estro14:*
96: em_estro15:*
97: em_estro16:*
98: em_estro17:*
99: em_estro18:*
100: em_estro19:*
101: em_estro20:*
102: gb_est25:*
103: gb_est26:*
104: gb_est27:*
105: gb_est28:*
106: gb_est29:*
107: gb_est30:*
108: gb_est31:*
109: gb_est32:*
110: gb_est41:*
111: gb_est42:*
112: gb_est43:*
113: gb_est44:*
114: gb_est45:*
115: gb_est46:*
116: gb_est47:*

117: gb_est48:*
118: gb_est49:*
119: gb_est50:*
120: gb_est51:*
121: gb_est52:*
122: gb_est53:*
123: gb_est54:*
124: gb_est55:*
125: gb_est56:*
126: gb_est57:*
127: gb_est58:*
128: gb_est59:*
129: gb_est60:*
130: gb_est61:*
131: gb_est62:*
132: gb_est63:*
133: gb_est64:*
134: gb_est65:*
135: gb_est66:*
136: gb_est67:*
137: gb_est76:*
138: gb_est77:*
139: gb_est78:*
140: gb_est79:*
141: gb_est80:*
142: gb_est81:*
143: gb_est82:*
144: gb_est83:*
145: gb_est84:*
146: gb_est85:*
147: gb_est86:*
148: gb_est87:*
149: gb_est88:*
150: gb_est89:*
151: gb_est90:*
152: gb_est99:*
153: gb_est100:*
154: gb_est101:*
155: gb_est102:*
156: gb_est103:*
157: gb_est104:*
158: gb_est105:*
159: gb_est106:*
160: gb_est67:*
161: gb_est68:*
162: gb_est69:*
163: gb_est70:*
164: gb_est71:*
165: gb_est72:*
166: gb_est73:*
167: gb_est74:*
168: gb_est91:*
169: gb_est92:*
170: gb_est93:*
171: gb_est94:*
172: gb_est95:*
173: gb_est96:*
174: gb_est97:*
175: gb_est98:*
176: em_esthum29:*
177: em_esthum30:*
178: em_esthum31:*
179: em_esthum32:*
180: em_esthum33:*
181: em_estom3:*
182: em_estpl11:*
183: em_estro21:*
184: em_estro22:*
185: em_estro23:*
186: em_htc:*
187: gb_est107:*
188: gb_est108:*
189: gb_est109:*

190: gb_est110:*
191: gb_est111:*
192: gb_htc:*
193: em_gss_fun:*
194: em_gss_hum1:*
195: em_gss_hum2:*
196: em_gss_hum3:*
197: em_gss_hum4:*
198: em_gss_hum5:*
199: em_gss_hum6:*
200: em_gss_hum7:*
201: em_gss_hum8:*
202: em_gss_hum9:*
203: em_gss_inv1:*
204: em_gss_inv2:*
205: em_gss_inv3:*
206: em_gss_other:*
207: em_gss_pln1:*
208: em_gss_pln2:*
209: em_gss_pro:*
210: em_gss_rod1:*
211: em_gss_rod2:*
212: em_gss_rod3:*
213: em_gss_rod4:*
214: em_gss_rod5:*
215: em_gss_vrt1:*
216: em_gss_vrt2:*
217: em_gss_vrt3:*
218: gb_gss1:*
219: gb_gss2:*
220: gb_gss3:*
221: gb_gss4:*
222: gb_gss5:*
223: gb_gss6:*
224: gb_gss7:*
225: gb_gss8:*
226: gb_gss9:*
227: gb_gss10:*
228: gb_gss11:*
229: gb_gss12:*
230: gb_gss13:*
231: gb_gss14:*
232: gb_gss15:*
233: gb_gss16:*
234: gb_gss17:*
235: gb_gss18:*
236: gb_gss19:*
237: gb_gss20:*
238: gb_gss21:*
239: gb_gss22:*
240: gb_gss23:*
241: gb_gss24:*
242: gb_gss25:*
243: gb_gss26:*
244: gb_gss27:*
245: gb_gss28:*
246: gb_gss29:*
247: gb_gss30:*
248: gb_gss31:*
249: gb_gss32:*
250: gb_gss33:*
251: gb_gss34:*
252: em_gss_inv4:*
253: em_gss_rod6:*
254: em_gss_rod7:*
255: em_gss_rod8:*
256: gb_gss35:*
257: gb_gss36:*
258: gb_gss37:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.


```
/note="putative"
/codon_start=1
/protein_id="BAB25115.1"
/db_xref="GI:12841203"
/translacion="MEMMRGRVGLGLVRLLAFLVGYQYPIPDSPSLQFGGQ
VRORYLYTDDQDETAHLEIREDTGVVGAARSPSELELLEKALKPGVQILGVKASRF
LCQOPDGLXGSPHFDPACSEFRELLEDEYNYVQSEHGLPLRLPKQSPNQDATSW
GPVRFPLMPGLLHPDQAGFLPPEPPDVSSDPLSNVPELQSRSPYAS"
BASE COUNT      204 a 278 c 241 g 227 t
ORIGIN
Query Match      98.4%; Score 638.4; DB 192; Length 950;
Best Local Similarity 99.8%; Pred. No. 9.3e-157;
Matches 639; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 atggaaatgagatcagatgttggaacctgggaactgtgggtccgactctgtgctt 60
DB 185 ATGGAATGGATGAGATCTAGAGTTGGGACCTGGGACTGTGGTCCGACTCTGCTGCT 244
QY 61 gtcttcctgctgggggtctaccaagcatacccccctccctgactccagccccctcccoag 120
DB 245 GTCCTTCTGCTGGGGTCTACCAAGCATACCCATCCCTGACTCCAGCCCTCTCCAG 304
QY 121 ttgggggtcgaagtcggcagaggtacctctacacagatgacagcaaacacacgaagcc 180
DB 305 TTTGGGGTCAAGTCCGCGAGAGTACCTCTACAGATGACGACCAAGACACTGAAGCC 364
QY 181 cacttgagatcagggagatgaaacagtgttagcgcagcacacccgcagtcagaaagt 240
DB 365 CACCTGGAGATCAGGAGGATGGAACATGTGTAGCGGAGCACACCCGAGTCCAGAAAT 424
QY 241 ctctggagctcaaaagccttgaagccaggggtcattcaaatcctcgggtgtcgaagcctct 300
DB 425 CTCTGGAGCTCAAAAGCCTTGAAGCCAGGGGTCAATCAAACTCTGGGTGTCAAAGCCTCT 484
QY 301 aggtttcttgccaacagccagatgagctctctatgagtcgctcactttgatcctgag 360
DB 485 AGGTTTCTTGGCAACAGCCAGATGGAGCTCTCTATGATGCGCTCACTTTGATCCTGAG 544
QY 361 gctgcagcttcagagaactctgtctggagagcgtttacaatgtgtaccagctctgaagcc 420
DB 545 GCCTGCAGCTTCAGAGAAGTCTGTCTGGAGGACGTTACATGTGTACCACTCTGAAGCC 604
QY 421 catggcctgcccctcgctgtgctcagaaaggaactcccccaaccaggatgcacatcctcgg 480
DB 605 CATGGCTGCCCTGCTGCTGCTCAGAGGACTCCCCAAACCAAGATGCAACATCTCTGG 664
QY 481 ggaactgtgcgttctgctccatgcagcctgtctccagagccccaagacacagcagga 540
DB 665 GGACCTGTGCGCTTCTGCTCCATGTCAGGCTGTCTCCAGAGCCCAAGACCAAGCAGGA 724
QY 541 ttctctgccccagagccccagatgtgggctcctctgacccccctgagcatggtgagcct 600
DB 725 TTCCTGCCCCAGAGCCGCCACCATGTGGGCTCTCTGACCCCTGAGCATGATGATGAGCCT 784
QY 601 ttacagggccgaagccccagctatgctgctgactctttc 640
DB 785 TTACAGGGCCGAAGCCCAAGCTATGCTGCTGACTCTTCC 824
RESULT 2
AV050323 310 bp mRNA EST 22-JUN-1999
LOCUS AV050323 Mus musculus pancreas C57BL/6J adult Mus musculus cDNA
DEFINITION clone 1810013H18, mRNA sequence.
ACCESSION AV050323
VERSION AV050323.1 GI:5136095
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1
REFERENCE 1 (bases 1 to 310)
Carninci, P., Shibata, K., Ozawa, Y., Konno, H., Itoh, M., Aizawa, K.,
Akahira, S., Akiyama, J., Fukuda, S., Fukunishi, Y., Funayama, T., Hara
, A., Hayatsu, N., Hori, F., Ishikawa, T., Itoh, M., Izawa, M., Kawai, J.,
Kikuchi, N., Kojima, Y., Matsuyama, T., Nitsuma, H., Oda, H., Owa, C.,
Sato, K., Shibata, Y., Shigemoto, Y., Shiraki, T., Sogabe, Y., Sugahara
, Y., Suzuki, H., Suzuki, H., Tateno, M., Tomaru, Y., Tomimaga, N.,
Watanabe, S., Yagame, M., Yamamura, T., Yokota, T., Yoshino, M.,
Muramatsu, M., Okazaki, Y. and Hayashizaki, Y.
RIKEN Mouse ESTs
Unpublished (1999)
Contact: Chie Owa
Genome Science Laboratory
RIKEN
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: 81-298-36-9145
Fax: 81-298-36-9098
Email: genome-res@rtc.riken.go.jp
Thermostabilization and thermoactivation of thermostable enzymes by
trehalose and its application for the synthesis of full length cDNA
(Proc. Natl. Acad. Sci. U.S.A. 95(2):520-524 (1998))
Transcriptional sequencing: A method for DNA sequencing using RNA
polymerase (Proc. Natl. Acad. Sci. U.S.A. 95(7):3455-3460 (1998))
Please visit our web site (http://genome.rtc.riken.go.jp) for
further details.
FEATURES
Location/Qualifiers
source
1..310
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="1810013H18"
/clone_lib="Mus musculus pancreas C57BL/6J adult"
/sex="male"
/tissue_type="pancreas"
/dev_stage="adult"
BASE COUNT 66 a 72 c 67 g 105 t
ORIGIN
Query Match 28.0%; Score 181.6; DB 109; Length 310;
Best Local Similarity 93.1%; Pred. No. 3.5e-37;
Matches 190; Conservative 0; Mismatches 14; Indels 0; Gaps 0;
QY 437 gtctgctcagaaggactccccaaaccagatgcaacatcctgggagcctgtgcgcttc 496
DB 1 GTCGCTTCAGAGGACTCCCAACCAAGCATGCAAAATCTCGGACATGTCGGATTCT 60
QY 497 tgccatgctcagggctgctccacgagcccccaagaccagagattcctgccccagagc 556
DB 61 TGCCCATGCCAGGCTTGTTCACGAGCCCAAGACCAAGCAGGATTCCTGCCCCAGAGC 120
QY 557 cccagatgtggctcctctgacccccctgagcatggtagagcctttacagggccgaagcc 616
DB 121 CCCAGATGTGGTCTTTTGGCCCCCTGAGCATGTGTAGAGCCTTTACAGGGCCGAAGCC 180
QY 617 ccagctatgctcctgactcttcc 640
DB 181 CCAGCTATGCTCTCTGAATTTTC 204
RESULT 3
AV049138 307 bp mRNA EST 22-JUN-1999
LOCUS AV049138 Mus musculus pancreas C57BL/6J adult Mus musculus cDNA
DEFINITION clone 1810008N24, mRNA sequence.
ACCESSION AV049138
VERSION AV049138.1 GI:5134910
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 307)
REFERENCE 1
```

AUTHORS

Carninci, P., Shibata, K., Ozawa, Y., Konno, H., Itoh, M., Aizawa, K., Akahira, S., Akiyama, J., Fukuda, S., Fukunishi, Y., Funayama, T., Hara, A., Hayatsu, N., Hori, F., Ishikawa, T., Itoh, M., Izawa, M., Kawai, J., Kikuchi, N., Kojima, Y., Matsuyama, T., Niitsuma, H., Oda, H., Owa, C., Sato, K., Shibata, Y., Shigemoto, Y., Shiraki, T., Sogabe, Y., Sugahara, Y., Suzuki, H., Suzuki, H., Tateno, M., Tomaru, Y., Tominaga, N., Watanabe, S., Yagame, M., Yamamura, T., Yokota, T., Yoshino, M., Muramatsu, M., Okazaki, Y. and Hayashizaki, Y.

TITLE

RIKEN Mouse ESTs

JOURNAL

Unpublished (1999)

COMMENT

Contact: Chie Owa

Genome Science Laboratory

RIKEN

3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan

Tel: 81-298-36-9145

Fax: 81-298-36-9098

Email: genome-res@rtc.riken.go.jp

Thermostabilization and thermoactivation of thermolabile enzymes by trehalose and its application for the synthesis of full length cDNA (Proc. Natl. Acad. Sci. U.S.A. 95(2):520-524 (1998))
Transcriptional sequencing: A method for DNA sequencing using RNA polymerase (Proc. Natl. Acad. Sci. U.S.A. 95(7):3455-3460 (1998))
Please visit our web site (<http://genome.rtc.riken.go.jp>) for further details.

FEATURES

source

Location/Qualifiers
1. .307

/organism="Mus musculus"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="1810008N24"

/clone_lib="Mus musculus pancreas C57BL/6J adult"

/sex="male"

/tissue_type="pancreas"

/dev_stage="adult"

65 a 72 c 67 g 103 t

BASE COUNT

ORIGIN

Query Match

Best Local Similarity 27.8%; Score 180.2; DB 109; Length 307;

Matches 188; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 440

tgctcagaaggactcccaaacaggatgcaacatctctgggacctgtgcttctgc 499

||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 1 TGCCTTAGAAGGATCCCAAAACAGGATGCAACATCTGGGGACCTGTGCGCTCTGCG 60

||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 500 ccattgcaggctctccagagcccaagcaagcagattccctgccccagagccccc 559

||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 61 CCATGGCAGGCCTATTATAGAGCCCAAGCAAGCAGGATTCCTGCCCCCAGAGCCCC 120

||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 560 cagatgtggtctctctgacccctgagcatggttagagcctttacagggccgaagcccca 619

||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 121 CAGATGTGGGATCTTTTGACCCCTGAGCATGTGATAGCCTTTACAGGCGCGAGCCCCA 180

||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 620 gctatgctctgactctttc 640

||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 181 GCTATGCTCTGATTTTTC 201

||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 4

AV050161

LOCUS

AV050161 301 bp mRNA EST 22-JUN-1999

DEFINITION AV050161 Mus musculus pancreas C57BL/6J adult Mus musculus cDNA

clone 1810012018, mRNA sequence.

ACCESSION AV050161

VERSION AV050161.1 GI:5135933

KEYWORDS EST.

SOURCE house mouse.

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 301)

REFERENCE Carninci, P., Shibata, K., Ozawa, Y., Konno, H., Itoh, M., Aizawa, K.,

Akahira, S., Akiyama, J., Fukuda, S., Fukunishi, Y., Funayama, T., Hara

TITLE

RIKEN Mouse ESTs

JOURNAL

Unpublished (1999)

COMMENT

Contact: Chie Owa

Genome Science Laboratory

RIKEN

3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan

Tel: 81-298-36-9145

Fax: 81-298-36-9098

Email: genome-res@rtc.riken.go.jp

Thermostabilization and thermoactivation of thermolabile enzymes by trehalose and its application for the synthesis of full length cDNA (Proc. Natl. Acad. Sci. U.S.A. 95(2):520-524 (1998))
Transcriptional sequencing: A method for DNA sequencing using RNA polymerase (Proc. Natl. Acad. Sci. U.S.A. 95(7):3455-3460 (1998))
Please visit our web site (<http://genome.rtc.riken.go.jp>) for further details.

FEATURES

source

Location/Qualifiers
1. .301

/organism="Mus musculus"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="1810012018"

/clone_lib="Mus musculus pancreas C57BL/6J adult"

/sex="male"

/tissue_type="pancreas"

/dev_stage="adult"

63 a 70 c 65 g 103 t

BASE COUNT

ORIGIN

Query Match

Best Local Similarity 24.9%; Score 161.4; DB 109; Length 301;

Matches 176; Conservative 0; Mismatches 6; Indels 1; Gaps 1;

QY 467

atgcacatctctggggacctgtgccttctctgccatgccagggctgtctcacagagcccc 526

||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 1 ATGCAACATACCTGGGGACCTGTGCGCTCTTGTGCCATGCCAGGCCTGTCCACGAGCCCC 60

||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 527 aagaccaagcagattctctgccccagagccccagatgtggctctctgacccctga 586

||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 61 AAGACCAAGCAGGATTCCTGCCCCCAGAGCCCCCAGAGTGTGGTTCCTTTGACCCCTGGA 120

||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 587 gcattgtagagcctttacaggccgaaagcccgatgcctctgactcttctctgaat 646

||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 121 GCATGTAGAGCCTTTACAGGCGCGAGCCCCCAGCTATGCGTCTGA-TTTTCTCTGAAT 179

||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 647 cta 649

||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 180 CTA 182

||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 5

AV060326

LOCUS

AV060326 278 bp mRNA EST 23-JUN-1999

DEFINITION AV060326 Mus musculus pancreas C57BL/6J adult Mus musculus cDNA

clone 1810062H22, mRNA sequence.

ACCESSION AV060326

VERSION AV060326.1 GI:5160073

KEYWORDS EST.

SOURCE house mouse.

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 278)

REFERENCE Carninci, P., Shibata, K., Ozawa, Y., Konno, H., Itoh, M., Aizawa, K.,

Akahira, S., Akiyama, J., Fukuda, S., Fukunishi, Y., Funayama, T., Hara

A., Hayatsu, N., Hori, F., Ishikawa, T., Itoh, M., Izawa, M., Kawai, J., Kikuchi, N., Kojima, Y., Matsuyama, T., Nitsuma, H., Oda, H., Owa, C., Sato, K., Shibata, Y., Shigemoto, Y., Shiraki, T., Sogabe, Y., Sugahara, Y., Suzuki, H., Tateno, M., Tomaru, Y., Tominaga, N., Watanabe, S., Yagame, M., Yamamura, T., Yokota, T., Yoshino, M., Muramatsu, M., Okazaki, Y. and Hayashizaki, Y.

TITLE JOURNAL COMMENT

RIKEN Mouse ESTs
Unpublished (1999)
Contact: Chie Owa

Genome Science Laboratory
RIKEN

3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan

Tel.: 81-298-36-9145

Fax: 81-298-36-9098

Email: genome-res@rtc.riken.go.jp

Thermostabilization and thermoactivation of thermolabile enzymes by trehalose and its application for the synthesis of full length cDNA (Proc. Natl. Acad. Sci. U.S.A. 95(2):520-524 (1998))

Transcriptional sequencing: A method for DNA sequencing using RNA polymerase (Proc. Natl. Acad. Sci. U.S.A. 95(7):3455-3460 (1998))

Please visit our web site (<http://genome.rtc.riken.go.jp>) for further details.

FEATURES

source

Location/Qualifiers

1..278

/organism="Mus musculus"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="1810062H22"

/clone_lib="Mus musculus pancreas C57BL/6J adult"

/sex="male"

/tissue_type="pancreas"

/dev_stage="adult"

54 a 69 c 62 g 93 t

BASE COUNT

ORIGIN

Query Match 22.8%; Score 148.2; DB 109; Length 278;

Best Local Similarity 95.0%; Pred. No. 1.9e-28;

Matches 153; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 480 gggacctgtgccttcctgcctccagggcgtctccacagagcccaagcagcagg 539

||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 12 GGGACCTGTGCGGTTCCTCCATCCAGGCGCTGTCCAGCAGCCCAAGCAGG 71

QY 540 attctgtcccccagagcccccagatgtggtctctgacccctgacatgtagacc 599

||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 72 ATTCTGCCCCCAGAGCCCCCAGATGTGGATCATTTGACCCCTGAGCATGGTAGGCC 131

QY 600 tttaggggcccgaagcccagctatgcgtcctgactcttc 640

||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 132 TTTACAGGCGCAGCCAGCCAGCTATGCGTCTGATCTCTCC 172

RESULT 6

AV052213

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

AV052213 Mus musculus pancreas C57BL/6J adult Mus musculus CDNA
clone 1810021E04, mRNA sequence.
EST.
house mouse.
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 288)

Carninci, P., Shibata, K., Ozawa, Y., Konno, H., Itoh, M., Aizawa, K., Akahira, S., Akiyama, J., Fukuda, S., Fukunishi, Y., Funayama, T., Hara, A., Hayatsu, N., Hori, F., Ishikawa, T., Itoh, M., Izawa, M., Kawai, J., Kikuchi, N., Kojima, Y., Matsuyama, T., Nitsuma, H., Oda, H., Owa, C., Sato, K., Shibata, Y., Shigemoto, Y., Shiraki, T., Sogabe, Y., Sugahara, Y., Suzuki, H., Tateno, M., Tomaru, Y., Tominaga, N., Watanabe, S., Yagame, M., Yamamura, T., Yokota, T., Yoshino, M.,

Muramatsu, M., Okazaki, Y. and Hayashizaki, Y.

RIKEN Mouse ESTs

Unpublished (1999)

Contact: Chie Owa

Genome Science Laboratory

RIKEN

3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan

Tel.: 81-298-36-9145

Fax: 81-298-36-9098

Email: genome-res@rtc.riken.go.jp

Thermostabilization and thermoactivation of thermolabile enzymes by trehalose and its application for the synthesis of full length cDNA (Proc. Natl. Acad. Sci. U.S.A. 95(2):520-524 (1998))

Transcriptional sequencing: A method for DNA sequencing using RNA polymerase (Proc. Natl. Acad. Sci. U.S.A. 95(7):3455-3460 (1998))

Please visit our web site (<http://genome.rtc.riken.go.jp>) for further details.

FEATURES

source

Location/Qualifiers

1..288

/organism="Mus musculus"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="1810021E04"

/clone_lib="Mus musculus pancreas C57BL/6J adult"

/sex="male"

/tissue_type="pancreas"

/dev_stage="adult"

62 a 65 c 61 g 100 t

BASE COUNT

ORIGIN

Query Match 22.8%; Score 148; DB 109; Length 288;

Best Local Similarity 96.8%; Pred. No. 2.2e-28;

Matches 151; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 485 ctgtgccttcctgcctccagggcgtctccacagagcccaagcagcaggattcc 544

||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 1 CTGTGCGCTTCCTGCCATCCAGGCGCTGATCCAGGCCCAAGCAGGAGGATTC 60

QY 545 tgccccagagccccagatgtgggtctctgacccctgagcagcagcattac 604

||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 61 TGCCCCCAGAGCCCCAGATGTGGTTCCTCTGACCCCTGAGCATGGTAGCCCTTAC 120

QY 605 agggcgaagcccagcgtatgcgtcctgactcttc 640

||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 121 AGGCCGAGCCCGAGCTATGCGTCTGATTTTTC 156

RESULT 7

AV048437

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

AV048437 308 bp mRNA EST 22-JUN-1999
AV048437 Mus musculus pancreas C57BL/6J adult Mus musculus CDNA
clone 1810005124, mRNA sequence.
EST.
house mouse.
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 308)

Carninci, P., Shibata, K., Ozawa, Y., Konno, H., Itoh, M., Aizawa, K., Akahira, S., Akiyama, J., Fukuda, S., Fukunishi, Y., Funayama, T., Hara, A., Hayatsu, N., Hori, F., Ishikawa, T., Itoh, M., Izawa, M., Kawai, J., Kikuchi, N., Kojima, Y., Matsuyama, T., Nitsuma, H., Oda, H., Owa, C., Sato, K., Shibata, Y., Shigemoto, Y., Shiraki, T., Sogabe, Y., Sugahara, Y., Suzuki, H., Tateno, M., Tomaru, Y., Tominaga, N., Watanabe, S., Yagame, M., Yamamura, T., Yokota, T., Yoshino, M.,

Muramatsu, M., Okazaki, Y. and Hayashizaki, Y.
RIKEN Mouse ESTs
Unpublished (1999)
Contact: Chie Owa

Genome Science Laboratory

trehalose and its application for the synthesis of full length cDNA (Proc. Natl. Acad. Sci. U.S.A. 95(2):520-524 (1998))
Transcriptional sequencing: A method for DNA sequencing using RNA polymerase (Proc. Natl. Acad. Sci. U.S.A. 95(7):3455-3460 (1998))
Please visit our web site (<http://genome.rtc.riken.go.jp>) for further details.

FEATURES

Location/Qualifiers
1..272
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="1810045M15"
/clone_lib="Mus musculus pancreas C57BL/6J adult"
/sex="male"
/tissue_type="pancreas"
/dev_stage="adult"

BASE COUNT 60 a 55 c 54 g 103 t
ORIGIN

Query Match 17.8%; Score 115.2; DB 109; Length 272;
Best Local Similarity 93.6%; Pred. No. 8.5e-20;
Matches 131; Conservative 0; Mismatches 8; Indels 1; Gaps 1;

QY 510 cctgtccacgagcccaagacagcaggtctctgcccagagcccccagatgtggg 569
Db 10 CTGTGTACTGTGAGCCCAAGACCAAGCAGGATTCATGCCCCAGAGCCCCAGATGTGGG 69

QY 570 ctcctctgacccctgagcatgttagagcctttacagggccgaagcccccagctgcgc 629
Db 70 CTCCTCTGACCCCTGAGCATGTGATGAGCCTTTACAGGGCCGAGCCCGAGCTATGCGTC 129

QY 630 ctgactcttctcgaatcta 649
Db 130 CTGA-TTTTCTCTGAATCTA 148

RESULT 10

AV052248 272 bp mRNA EST 22-JUN-1999
LOCUS AV052248 Mus musculus pancreas C57BL/6J adult Mus musculus cDNA
DEFINITION clone 1810021F21, mRNA sequence.

ACCESSION AV052248.1 GI:5138020
VERSION
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 272)

AUTHORS Carninci, P., Shibata, K., Ozawa, Y., Konno, H., Itoh, M., Aizawa, K., Akahira, S., Akiyama, J., Fukuda, S., Fukunishi, Y., Funayama, T., Hara, A., Hayatsu, N., Hori, F., Ishikawa, T., Itoh, M., Izawa, M., Kawai, J., Kikuchi, N., Kojima, Y., Matsuyama, T., Naitsuma, H., Oda, H., Owa, C., Sato, K., Shibata, Y., Shigemoto, Y., Shiraki, T., Sogabe, Y., Sugahara, Y., Suzuki, H., Suzuki, H., Tateno, M., Tomaru, Y., Tomimaga, N., Watanabe, S., Yagame, M., Yamamura, T., Yokota, T., Yoshino, M., Muramatsu, M., Okazaki, Y. and Hayashizaki, Y.

TITLE

RIKEN Mouse ESTs

Unpublished (1999)

Contact: Chie Owa

Genome Science Laboratory

RIKEN

3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan

Tel: 81-298-36-9145

Fax: 81-298-36-9098

Email: genome-resertrc.riken.go.jp

Thermostabilization and thermoactivation of thermolabile enzymes by trehalose and its application for the synthesis of full length cDNA (Proc. Natl. Acad. Sci. U.S.A. 95(2):520-524 (1998))

Transcriptional sequencing: A method for DNA sequencing using RNA polymerase (Proc. Natl. Acad. Sci. U.S.A. 95(7):3455-3460 (1998))

Please visit our web site (<http://genome.rtc.riken.go.jp>) for

FEATURES
source
Location/Qualifiers
1..272
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="1810021F21"
/clone_lib="Mus musculus pancreas C57BL/6J adult"
/sex="male"
/tissue_type="pancreas"
/dev_stage="adult"

BASE COUNT 54 a 60 c 53 g 105 t
ORIGIN

Query Match 17.5%; Score 113.4; DB 109; Length 272;
Best Local Similarity 88.5%; Pred. No. 2.5e-19;
Matches 123; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY 502 atgccagcctgtccacgagcccaagacagcaggtctctgcccagagcccccagagccccc 561
Db 6 ATTCAGGCCCTGTTTAAACGAGCCCAAGACCAAGCAGGATTCCTGCCCTGAGCCCCCA 65

QY 562 gatgtgctctctgtacccctgagcatgttagagcctttacagggccgaagcccccagc 621
Db 66 GATTGTGGCTCCTCTGACCCCTTGAGCATGTGATGAGCCTTTACAGGGCCGAGCCCGAGC 125

QY 622 tatgctctcgaactcttc 640
Db 126 TATGCTTCTCTGAATTTTCC 144

RESULT 11

LOCUS AQ175436 496 bp DNA GSS 17-OCT-1998
DEFINITION HS_3207_Al_H09_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plates=3207 Col=17 Row=O, DNA sequence.

ACCESSION AQ175436.1 GI:3572803
VERSION
KEYWORDS GSS.
SOURCE human.

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 496)
Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T., Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and Hood, L.

REFERENCE Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome

Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)

JOURNAL

99380589

MEDLINE

Contact: Mahairas GG, Wallace JC, Hood L

High Throughput Sequencing Center

University of Washington

401 Queen Anne Avenue North, Seattle, WA 98109, USA

Tel: (206) 616-3618

Fax: (206) 616-3887

Email: jwallace@u.washington.edu

Sequence Tagged Connector

Plate: 3207 row: O column: 17

Class: BAC ends

High quality sequence stop: 496.

Location/Qualifiers
1..496

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="Plate=3207 Col=17 Row=O"

/clone_lib="CIT Approved Human Genomic Sperm Library D"

/sex="male"

/note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in E-Coli DH10B"

BASE COUNT 106 a 139 c 137 g 100 t 14 others


```

QY 616 ccagctatgcgtcctgactctttc 640
Db 66 CCCAGCTATGCGTCTCGAATTTC 90

RESULT 14
AV059644
LOCUS AV059644 190 bp mRNA EST 23-JUN-1999
DEFINITION AV059644 Mus musculus pancreas C57BL/6J adult Mus musculus cDNA
clone 1810059K10, mRNA sequence.
ACCESSION AV059644
VERSION AV059644.1 GI:5159391
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 190)
AUTHORS Akahira,S., Akiyama,J., Fukuda,S., Fukunishi,Y., Funayama,T., Hara
,A., Hayatsu,N., Hori,F., Ishikawa,T., Itoh,M., Izawa,M., Kawai,J.,
Kikuchi,N., Kojima,Y., Matsuyama,T., Niitsuma,H., Oda,H., Owa,C.,
Sato,K., Shibata,Y., Shigemoto,Y., Shiraki,T., Sogabe,Y., Sugahara
,Y., Suzuki,H., Suzuki,H., Tateno,M., Tomaru,Y., Tominaga,N.,
Watanabe,S., Yagame,M., Yamamura,T., Yokota,T., Yoshino,M.,
Muramatsu,M., Okazaki,Y. and Hayashizaki,Y.
RIKEN Mouse ESTs
JOURNAL Unpublished (1999)
COMMENT Contact: Chie Owa
Genome Science Laboratory
RIKEN
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: 81-298-36-9145
Fax: 81-298-36-9098
Email: genome-resetc.riken.go.jp
Thermostabilization and thermoactivation of thermolabile enzymes by
trehalose and its application for the synthesis of full length cDNA
(Proc. Natl. Acad. Sci. U.S.A. 95(2):520-524 (1998))
Transcriptional sequencing: A method for DNA sequencing using RNA
polymerase (Proc. Natl. Acad. Sci. U.S.A. 95(7):3455-3460 (1998))
Please visit our web site (http://genome.ritc.riken.go.jp) for
further details.
FEATURES
source
Location/Qualifiers
1..190
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="1810059K10"
/tissue_type="pancreas"
/sex="male"
/dev_stage="adult"
BASE COUNT 35 a 45 c 35 g 75 t
ORIGIN
Query Match 8.7%; Score 56.6; DB 109; Length 190;
Best Local Similarity 88.0%; Pred. No. 0.00018;
Matches 73; Conservative 0; Mismatches 9; Indels 1; Gaps 1;
QY 559 ccagatggggctcctctgaccctga-gcatgttagagccttacaggccgaagccc 617
Db 12 CCAGATGACATCTCCTATGACCCCTCAGGCATGGTAGACCCCTACAGGCGCGAGCCC 71
QY 618 cagctatgcgtcctgactctttc 640
Db 72 CAGCTATGCGTCTCGACTCTTC 94

RESULT 15
BE869144
LOCUS BE869144 741 bp mRNA EST 20-OCT-2000

```

```

DEFINITION 601445130F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3849343 5',
mRNA sequence.
ACCESSION BE869144
VERSION BE869144.1 GI:10317920
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 741)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Place: LLN9566 row: k column: 08
High quality sequence stop: 696.
Location/Qualifiers
1..741
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3849343"
/tissue_type="NIH_MGC_65"
/lab_host="DH10B (phage-resistant)"
/notes="Organ: colon; Vector: pCMV-SPORT6; Site:1: NotI;
Site:2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.8 kb. Library constructed by Life
Technologies."
BASE COUNT 122 a 259 c 235 g 125 t
ORIGIN
Query Match 8.4%; Score 54.2; DB 141; Length 741;
Best Local Similarity 48.3%; Pred. No. 0.00097;
Matches 183; Conservative 0; Mismatches 193; Indels 3; Gaps 1;
QY 66 cctgtgggggtctaccagcataccctccctgactccagccctcctccagttgg 125
Db 166 CGTGCGCGGGCGCCCTCGCCTTCTCGGACGCGGGGCCCCACGTGCTACGCGGTGGG 225
QY 126 gggccaagtccggcagaggtacctctacacagatgacgacccaag---acactgaagccca 182
Db 226 CGACCCCATCCGCTGCGGCACCTGTACACCTCGGCCCCCAGGGCTCTCCAGCTGCTT 285
QY 183 cctggagatcaggggaggtggaaacagtggttagcgacgacacccagtcacgaagtct 242
Db 286 CCTGCGCATCCGTGCGGACGCGCTGTGACTGCTGCGGCGGGGCGGCGGCACAGTTT 345
QY 243 cctggagctcaaaagcctgaagccagggtcattcaaatcctgggtgtcaagcctctag 302
Db 346 GCTGGAGATCAAGGAGTAGTCGCTCTCGGGACCTGGCCATCAAGGGCGGTGCACAGGCGTGG 405
QY 303 gttcttttccaacagccagatggagctctctatggatgcgctcactttgatcctgagggc 362
Db 406 GTACTCTCATGTTGGCGCGACGCGCAAGATGTCAGGGGCTGCTTCAGTACTCGAGAGAGA 465
QY 363 ctgcagcttcacagaaactgctgctggagagcaggttacaatgtgtaccagttctgaagccca 422
Db 466 CTGTGCTTTTCGAGAGGAGATCCGCCAGATGGCTACAAATGTGTACCATCGGAGAGCA 525
QY 423 tggcctgcccctgcgtctg 441
Db 526 CCGCCTCCGGTCTCCCTG 544

```


Search completed: August 6, 2001, 21:43:05
Job time: 2701 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 6, 2001, 22:28:00 ; Search time 91.85 Seconds
(without alignments)
1337.647 Million cell updates/sec

Title: US-09-391-861-3

Perfect score: 649

Sequence: 1 atggaatgatgatgatctag.....ctgactcttctgaatcta 649

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 324599 seqs, 9465562 residues

Total number of hits satisfying chosen parameters: 649198

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_NA.*

- 1: /cgn2_6/prodata/1/ina/5A_COMB.seq.*
- 2: /cgn2_6/prodata/1/ina/5B_COMB.seq.*
- 3: /cgn2_6/prodata/1/ina/6A_COMB.seq.*
- 4: /cgn2_6/prodata/1/ina/6B_COMB.seq.*
- 5: /cgn2_6/prodata/1/ina/PCTUS_COMB.seq.*
- 6: /cgn2_6/prodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	35.4	5.5	725	PCT-US94-04361-21	Sequence 21, Appl
2	35.4	5.5	788	US-08-883-795A-35	Sequence 35, Appl
3	35.4	5.5	823	US-08-785-750-1	Sequence 1, Appl
4	35.4	5.5	1011	US-08-750-128-12	Sequence 12, Appl
5	35.4	5.5	3601	US-09-017-631-23	Sequence 23, Appl
6	35.4	5.5	3602	US-08-883-795A-33	Sequence 33, Appl
7	35.4	5.5	3602	US-09-018-138-1	Sequence 1, Appl
8	35.2	5.4	1864	US-08-454-720A-38	Sequence 38, Appl
9	33.4	5.1	5975	US-08-404-354B-1	Sequence 1, Appl
10	33.4	5.1	5975	US-08-314-083B-1	Sequence 1, Appl
11	33.4	5.1	5975	US-08-435-675B-1	Sequence 1, Appl
12	33.4	5.1	5975	US-08-884-599-1	Sequence 1, Appl
13	32.8	5.1	423	US-08-187-780-2	Sequence 2, Appl
14	32.8	5.1	423	US-08-187-780-5	Sequence 5, Appl
15	32.8	5.1	423	US-08-478-485-2	Sequence 2, Appl
16	32.8	5.1	423	US-08-478-485-5	Sequence 5, Appl
17	32.8	5.1	599	5430019-1	Patent No. 5430019
18	32.8	5.1	1219	PCT-US93-06251-11	Sequence 11, Appl
19	32.4	5.0	1656	US-09-026-958-1	Sequence 1, Appl
20	32.2	5.0	681	PCT-US94-04361-22	Sequence 22, Appl
21	32.2	5.0	681	PCT-US94-04361-27	Sequence 27, Appl
22	32.2	5.0	1288	US-08-440-856A-9	Sequence 9, Appl
23	32.2	5.0	5107	US-08-910-647-3	Sequence 3, Appl
24	31.8	4.9	5962	5386025-5	Patent No. 5386025
25	31.6	4.9	687	PCT-US94-04361-25	Sequence 25, Appl
26	31.6	4.9	3393	US-08-295-502-1	Sequence 1, Appl
27	31.6	4.9	3393	PCT-US95-10691-1	Sequence 1, Appl

28 31.6 4.9 4543 2 US-08-519-547A-5 Sequence 5, Appl
 29 31.2 4.8 750 3 US-09-010-809-12 Sequence 12, Appl
 30 31.2 4.8 1317 1 US-08-153-848-45 Sequence 45, Appl
 31 31.2 4.8 1317 3 US-09-299-843A-45 Sequence 45, Appl
 32 31.2 4.8 1317 5 PCT-US93-11153-45 Sequence 45, Appl
 33 31.2 4.8 1469 5 PCT-US92-08258-1 Sequence 1, Appl
 34 31.2 4.8 1737 1 US-08-202-056-4 Sequence 4, Appl
 35 31.2 4.8 1737 1 US-08-076-093A-3 Sequence 3, Appl
 36 31.2 4.8 1737 1 US-08-701-265-3 Sequence 3, Appl
 37 31.2 4.8 1737 2 US-08-284-586-3 Sequence 3, Appl
 38 31.2 4.8 1737 2 US-08-805-478-3 Sequence 3, Appl
 39 31.2 4.8 1737 2 US-08-802-627A-3 Sequence 3, Appl
 40 31.2 4.8 1737 2 US-08-801-238-3 Sequence 3, Appl
 41 31.2 4.8 1737 2 US-08-801-228-3 Sequence 3, Appl
 42 31.2 4.8 1737 3 US-09-104-296-3 Sequence 3, Appl
 43 31.2 4.8 1737 5 PCT-US94-06380-2 Sequence 2, Appl
 44 31.2 4.8 2129 1 US-08-426-819A-34 Sequence 34, Appl
 45 31.2 4.8 2138 3 US-08-776-271-1 Sequence 1, Appl

ALIGNMENTS

RESULT 1
 PCT-US94-04361-21
 ; Sequence 21, Application PC/TUS9404361
 ; GENERAL INFORMATION:
 ; APPLICANT: Brigham and Women's Hospital
 ; APPLICANT: 75 Francis Street
 ; APPLICANT: Boston, MA 02115
 ; APPLICANT: Bunn, H. Franklin
 ; APPLICANT: Wen, Danyi
 ; APPLICANT: Showers, Mark O.
 ; TITLE OF INVENTION: Erythropoietin Muteins With Enhanced
 ; TITLE OF INVENTION: Activity
 ; NUMBER OF SEQUENCES: 59
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
 ; STREET: 1100 New York Avenue, Suite 600
 ; CITY: Washington
 ; STATE: D.C.
 ; COUNTRY: U.S.A.
 ; ZIP: 20005-3934
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/US94/04361
 ; FILING DATE: Herewith
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/049,802
 ; FILING DATE: 21-APR-1993
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Cimbala, Michele A.
 ; REGISTRATION NUMBER: 33,851
 ; REFERENCE/DOCKET NUMBER: 0627.336PC01
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (202) 371-2600
 ; TELEFAX: (202) 371-2540
 ; INFORMATION FOR SEQ ID NO: 21:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 725 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: both
 ; PCT-US94-04361-21

Query Match 5.5%; Score 35.4; DB 5; Length 725;
 Best Local Similarity 57.8%; Pred. No. 0.33;


```
; STATE: VIRGINIA
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk, 3.50 inch.
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/750,128
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: IT FI 94 A 000106
; FILING DATE: 27-MAY-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Robert L. Price
; REGISTRATION NUMBER: 22,685
; REFERENCE/DOCKET NUMBER: 2879-007
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-684-1111
; TELEFAX: 703-684-1124
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1011 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; US-08-750-128-12

Query Match          5.5%; Score 35.4; DB 2; Length 1011;
Best Local Similarity 57.8%; Pred. No. 0.38;
Matches 63; Conservative 0; Mismatches 46; Indels 0; Gaps 0;

QY 43 gtccgactgtcgtgcttctctgctggtggttcacacgatacccatccctgac 102
Db 22 GCGTGGCTGTGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 81

QY 103 tccagcccccctcctcagtttggtggttcacacgatacccatccctgac 151
Db 82 GCCCACCACCGCTCATCTGTGACACGCGAGTCTCTGGAGAGGTACCTCT 130

RESULT 5
US-09-017-631-23
; Sequence 23, Application US/09017631B
; Patent No. 6153407
; GENERAL INFORMATION:
; APPLICANT: Sytkowski, Arthur J.
; TITLE OF INVENTION: ERYTHROPOIETIN WITH ALTERED BIOLOGICAL
; FILE REFERENCE: NEDH92-04A22A
; CURRENT APPLICATION NUMBER: US/09/017,631B
; EARLIER FILING DATE: 1998-02-03
; EARLIER APPLICATION NUMBER: US 08/808,881
; EARLIER FILING DATE: 1997-02-28
; EARLIER APPLICATION NUMBER: US 08/383,743
; EARLIER FILING DATE: 1995-02-02
; EARLIER APPLICATION NUMBER: US 08/113,080
; EARLIER FILING DATE: 1993-08-26
; EARLIER APPLICATION NUMBER: US 07/920,810
; EARLIER FILING DATE: 1992-07-28
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 23
; LENGTH: 3601
; TYPE: DNA
; ORGANISM: Homo sapien
; US-09-017-631-23

Query Match          5.5%; Score 35.4; DB 2; Length 1011;
Best Local Similarity 57.8%; Pred. No. 0.38;
Matches 63; Conservative 0; Mismatches 46; Indels 0; Gaps 0;

QY 43 gtccgactgtcgtgcttctctgctggtggttcacacgatacccatccctgac 102
Db 22 GCGTGGCTGTGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 81

QY 103 tccagcccccctcctcagtttggtggttcacacgatacccatccctgac 151
Db 82 GCCCACCACCGCTCATCTGTGACACGCGAGTCTCTGGAGAGGTACCTCT 130

RESULT 5
US-09-017-631-23
; Sequence 23, Application US/09017631B
; Patent No. 6153407
; GENERAL INFORMATION:
; APPLICANT: Sytkowski, Arthur J.
; TITLE OF INVENTION: ERYTHROPOIETIN WITH ALTERED BIOLOGICAL
; FILE REFERENCE: NEDH92-04A22A
; CURRENT APPLICATION NUMBER: US/09/017,631B
; EARLIER FILING DATE: 1998-02-03
; EARLIER APPLICATION NUMBER: US 08/808,881
; EARLIER FILING DATE: 1997-02-28
; EARLIER APPLICATION NUMBER: US 08/383,743
; EARLIER FILING DATE: 1995-02-02
; EARLIER APPLICATION NUMBER: US 08/113,080
; EARLIER FILING DATE: 1993-08-26
; EARLIER APPLICATION NUMBER: US 07/920,810
; EARLIER FILING DATE: 1992-07-28
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 23
; LENGTH: 3601
; TYPE: DNA
; ORGANISM: Homo sapien
; US-09-017-631-23

Query Match          5.5%; Score 35.4; DB 3; Length 3601;
Best Local Similarity 57.8%; Pred. No. 0.62;
Matches 63; Conservative 0; Mismatches 46; Indels 0; Gaps 0;

QY 43 gtccgactgtcgtgcttctctgctggtggttcacacgatacccatccctgac 102
Db 1208 gctcggtgtggttctctctgctggtggttcacacgatacccatccctgac 1267

QY 103 tccagcccccctcctcagtttggtggttcacacgatacccatccctgac 151
Db 1268 gcccccaccgacctctgtgacagccgagctctctggagaggtacctct 1316

RESULT 6
US-08-883-795A-33
; Sequence 33, Application US/08883795A
; Patent No. 5985607
; GENERAL INFORMATION:
; APPLICANT: Delcuve, Genevieve
; TITLE OF INVENTION: Recombinant DNA Molecules and Expression
; TITLE OF INVENTION: Vectors for Tissue Plasminogen Activator
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BERESKIN & PARR
; STREET: 40 King Street West
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5H 3Y2
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/883,795A
; FILING DATE: 27-JUN-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Gravelle, Micheline
; REGISTRATION NUMBER: 40,261
; REFERENCE/DOCKET NUMBER: 7841-062
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 364-7311
; TELEFAX: (416) 361-1398
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3602 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: join(625..637, 1201..1346, 1605..1691, 2303..2482,
; LOCATION: 2617..2772)
; FEATURE:
; NAME/KEY: mRNA
; LOCATION: join(625..637, 1201..1346, 1605..1691, 2303..2482,
; LOCATION: 2617..2772)
; US-08-883-795A-33

Query Match          5.5%; Score 35.4; DB 2; Length 3602;
Best Local Similarity 57.8%; Pred. No. 0.62;
Matches 63; Conservative 0; Mismatches 46; Indels 0; Gaps 0;

QY 43 gtccgactgtcgtgcttctctgctggtggttcacacgatacccatccctgac 102
```


TELECOMMUNICATION INFORMATION:

TELEPHONE: 619-238-0999
TELEFAX: 619-238-0062
TELEX:

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 5975 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

FEATURE:

NAME/KEY: Coding Sequence

LOCATION: 79...5700

OTHER INFORMATION:

US-08-404-354B-1

Query Match 5.1%; Score 33.4; DB 1; Length 5975;

Best Local Similarity 43.0%; Pred. No. 2.9;

Matches 163; Conservative 0; Mismatches 216; Indels 0; Gaps 0;

QY 29 cctggagactgtgggtcccaactgctgctgctgtcttctctgctgggggtctaccagcat 88

Db 3605 CCCCTGGCCTTGAACGCCAAGAGCTTGAGAAATCATCTCCAGCGTGAAGATGATGGTGAAG 3546

QY 89 acccctccctgactccagccccctccagtttgggggtcaagtcccgccagaggtacc 148

Db 3545 GCACATGAGGATGCTGAGATGTGTTTCATCTCCGACTGGGTAGTGTGCTGATG 3486

QY 149 tctacacagatgacgaccacactgaagccacactggagatcagggaggtgaaacag 208

Db 3485 CCCAGGCAGATGCTGTGACATGATGAGGGCGAAGCATCAGGTATTCAAAGTAGGAGGAG 3426

QY 209 tggtaggcgcagcacccgcagtcacgaagtctctgagctcaaaagccttgaagccag 268

Db 3425 GTGACGACGTACCACACCTGGTACTGGTATGGGTCTTTGGGGATCTAGCACCAGGTGGG 3366

QY 269 ggggtcattcaaatccctgggtgtcaagcctctaggtttcttgcacacgacagatggag 328

Db 3365 CGGGCCTTCAGGGCATACTGCACACTGGCGGTGCTTCTTGCCAGCTCGCAGTCTTG 3306

QY 329 ctctctatgagtcgctcaactttgactcctgagcctgcagcttcagaaactgctgctgg 388

Db 3305 TACTCCGCTCTCCCGCTCTCCTGGAAGGTGACGATGACAAAGCCCAAAAGATGTTTCATC 3246

QY 389 aggcaggttacaatgtga 407

Db 3245 ATGAAGAAGCAATGAGGA 3227

RESULT 10

US-08-314-083B-1/c

; Sequence 1, Application US/08314083B

; Patent No. 5686241

; GENERAL INFORMATION:

; APPLICANT: Ellis, Steven Bradley

; APPLICANT: Williams, Mark E.

; APPLICANT: Harpold, Michael Miller

; APPLICANT: Brenner, Robert

; APPLICANT: Schwartz, Arnold

; TITLE OF INVENTION: CALCIUM CHANNEL COMPOSITIONS AND METHODS

; NUMBER OF SEQUENCES: 3

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Brown, Martin, Haller & McClain

; STREET: 1660 Union Street

; CITY: San Diego

; STATE: CA

; COUNTRY: USA

; ZIP: 92101-2926

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq Version 1.5

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/314,083B

FILING DATE: 28-SEPT-1994

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/914,231

FILING DATE: 13-JUL-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/603,751

FILING DATE: 08-NOV-1990

ATTORNEY/AGENT INFORMATION:

NAME: Seidman, Stephanie L

REGISTRATION NUMBER: 33,779

REFERENCE/DOCKET NUMBER: 6362-53191

TELECOMMUNICATION INFORMATION:

TELEPHONE: 619-238-0999

TELEFAX: 619-238-0062

TELEX:

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 5975 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

FEATURE:

NAME/KEY: Coding Sequence

LOCATION: 79...5700

OTHER INFORMATION:

US-08-314-083B-1

Query Match 5.1%; Score 33.4; DB 1; Length 5975;

Best Local Similarity 43.0%; Pred. No. 2.9; Indels 0; Gaps 0;

Matches 163; Conservative 0; Mismatches 216; Indels 0; Gaps 0;

QY 29 cctggagactgtgggtcccaactgctgctgctgtcttctctgctgggggtctaccagcat 88

Db 3605 CCCCTGGCCTTGAACGCCAAGAGCTTGAGAAATCATCTCCAGCGTGAAGATGATGGTGAAG 3546

QY 89 acccctccctgactccagccccctccctccagtttgggggtcaagtcccgccagaggtacc 148

Db 3545 GCACATGAGGATGCTGAGATGTGTTTCATCTCCCGACTGGTGTGCTGCTGCTG 3486

QY 149 tctacacagatgacgaccacactgaagccacactggagatcagggaggtgaaacag 208

Db 3485 CCCAGGCAGATGCTGTGACATGATGAGGGCGAAGCATCAGGTATTCAAAGTAGGAGGAG 3426

QY 209 tggtaggcgcagcacccgcagtcacgaagtctctgagctcaaaagccttgaagccag 268

Db 3425 GTGACGACGTACCACACCTGGTACTGGTATGGGTCTTTGGGGATCTAGCACCAGGTGGG 3366

QY 269 ggggtcattcaaatccctgggtgtcaagcctctaggtttcttgcacacgacagatggag 328

Db 3365 CGGGCCTTCAGGGCATACTGCACACTGGCGGTGCTTCTTGCCAGCTCGCAGTCTTG 3306

QY 329 ctctctatgagtcgctcaactttgactcctgagcctgcagcttcagaaactgctgctgg 388

Db 3305 TACTCCGCTCTCCCGCTCTCCTGGAAGGTGACGATGACAAAGCCCAAAAGATGTTTCATC 3246

QY 389 aggcaggttacaatgtga 407

Db 3245 ATGAAGAAGCAATGAGGA 3227

RESULT 11

US-08-435-675B-1/c

; Sequence 1, Application US/08435675B

; Patent No. 5710250

; GENERAL INFORMATION:

; APPLICANT: Ellis, Steven Bradley

; APPLICANT: Williams, Mark E.
 ; APPLICANT: Harpold, Michael Miller
 ; APPLICANT: Schwartz, Arnold
 ; APPLICANT: Brenner, Robert
 ; TITLE OF INVENTION: CALCIUM CHANNEL COMPOSITIONS AND METHODS
 ; NUMBER OF SEQUENCES: 6
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Brown, Martin, Haller & McClain
 ; STREET: 1660 Union Street
 ; CITY: San Diego
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 92101-2926
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FastSEQ version 1.5
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/435,675B
 ; FILING DATE: 05-MAY-1995
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/314,083
 ; FILING DATE: 28-SEP-1994
 ; APPLICATION NUMBER: US 07/914,231
 ; FILING DATE: 13-JUL-1992
 ; APPLICATION NUMBER: US 07/603,751
 ; FILING DATE: 08-NOV-1990
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Seidman, Stephanie L
 ; REGISTRATION NUMBER: 33,779
 ; REFERENCE/DOCKET NUMBER: 6362-53193
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 619-238-0999
 ; TELEFAX: 619-238-0062
 ; TELEX:
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 5975 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cdna
 ; FEATURE:
 ; NAME/KEY: Coding Sequence
 ; LOCATION: 79...5700
 ; OTHER INFORMATION:
 ; US-08-435-675B-1

Query Match	5.1%	Score 33.4;	DB 1;	Length 5975;
Best Local Similarity	43.0%;	Pred. No. 2.9;		
Matches 163;	Conservative 0;	Mismatches 216;	Indels 0;	Gaps 0;

QY	29	cctcgggactggtgggtccgactgctgctgctgtcttcctcgtcgtggggtcaccagaat	88
Db	3605	CCCTGGCCTTGAA CGCCAGAGCTTGAGATCATCTCCACGCTGAAGATGATGGTGAAG	3546
QY	89	accccactcctgactccagccccctccctccagtttgggggtcgaagtcctggcagaggtacc	148
Db	3545	GCCACATTGAGGATGCTGAGATGTGGTTCATCTCCCGACTGGTGGTAGTCTGTCATG	3486
QY	149	tctacacagatgacgaccaaagacactgaagcccaactggagatcaggggaggtatggaacag	208
Db	3485	CCAGGACGATGGTGTGGAGCATGATGAGGCGCAACATCAGGTATTCAAGTAGGAGGAG	3426
QY	209	tgtgaggcgacgacacgcagtcacgaagctcctcggagctcaaaagccttgaagccag	268
Db	3425	GTGACGACGTACCA CACTGGTACTGTGTGGGTCTCTGGGGATGTAGCACCGAAGTGGG	3366
QY	269	gggtcattccaatcctcgggtgtcaaaagcctctaggtttttggccaacgaccagatggag	328

Db 3365 CGGGCCCTTCAGGCATACACTGACACACTGGCGCTGGTCTTCTTCCAGCTCCAGTTCCTTG 3306
 Qy 329 ctctctatggatcgctcactttgatccctgagggcctgcagcttcagagaaactgctgctg 388
 Db 3305 TACTCGCTCTCCCTTGCTCCTCGGAAGGTGAGATGACAAAGCCCAAGATGTTTCATC 3246
 Qy 389 aggacgggttacaatgtgta 407
 Db 3245 ATGAAGAAGGCAATGAGGA 3227
 RESULT 12
 US-08-884-599-1/c
 ; Sequence 1, Application US/08884599
 ; Patent No. 6013474
 ; GENERAL INFORMATION:
 ; APPLICANT: Ellis, Steven Bradley
 ; APPLICANT: Williams, Mark E.
 ; APPLICANT: Harpold, Michael Miller
 ; APPLICANT: Schwartz, Arnold
 ; APPLICANT: Brenner, Robert
 ; TITLE OF INVENTION: CALCIUM CHANNEL COMPOSITIONS AND METHODS
 ; NUMBER OF SEQUENCES: 3
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Brown, Martin, Haller & McClain
 ; STREET: 1660 Union Street
 ; CITY: San Diego
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 92101-2926
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FastSEQ Version 1.5
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/884,599
 ; FILING DATE: 27-JUNE-1997
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/314,083
 ; FILING DATE: 28-SEPT-1994
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/914,231
 ; FILING DATE: 13-JUL-1992
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/603,751
 ; FILING DATE: 08-NOV-1990
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Seidman, Stephanie L.
 ; REGISTRATION NUMBER: 33,779
 ; REFERENCE/DOCKET NUMBER: 6362-53191B
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 619-238-0999
 ; TELEFAX: 619-238-0062
 ; TELEX:
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 5975 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cDNA
 ; FEATURE:
 ; NAME/KEY: Coding Sequence
 ; LOCATION: 79...5700
 ; OTHER INFORMATION:
 ; US-08-884-599-1

Query Match 5.1%; Score 33.4; DB 3; Length 5975;
Best Local Similarity 43.0%; Pred. No. 2.9;
Matches 163; Conservative 0; Mismatches 216; Indels 0; Gaps 0;

QY 29 ccctggagactggtggccgactgctgctgtgtctctctgctgggggtctaccagcat 88
Db 3605 CCCCTGGCCTTGAACGCCAAGAGCTTGAAGATCATCTCCAGCGTGAAGATGATGGTGAAG 3546
QY 89 accccatccctgactccagccctccctccagtttgggggtcaagtccggcagaggtacc 148
Db 3545 GCCACATGTGAGGATGTGAGATGTGGTTCTCTCTCCGACTGGTGGTGTAGTCTGCATG 3486
QY 149 tctacacagatgagcagcaactgaagccacccactggagatcagggaggtggaacag 208
Db 3485 CCCAGGCAGATGGTGTGAGCATGATCAGCGCGAACAATCAGGTATTCAAAGTAGGAGGAG 3426
QY 209 tggtaggcagcagcaccgcagtcacagaaagtctctggagctcaagccttgaagccag 268
Db 3425 GTGACGACGTACACACCTGCTACTGTATGGTGTCTTGGGATGTAGCACCGAAGTGGG 3366
QY 269 ggtcattcaaatcctgggtgtcaaacctctaggtttcttttgcacagcagatggag 328
Db 3365 CGGCGCTTCAGGGGATACTGCACACACTGGCGTGGTGTCTTGTCCAGCTGCGCAGTCTTG 3306
QY 329 ctctctatggatgcctcactttgatctgagcctgcagcttcagagaaactgctgtg 388
Db 3305 TACTCCGCTCTCCCTCTCTCTGGAAGTGCAGTACCAAGCCACAAAGATGTTTCATC 3246
QY 389 agagcgttacaatgtgta 407
Db 3245 ATGAAGAAGGCAATGAGGA 3227

RESULT 13

US-08-187-780-2
; Sequence 2, Application US/08187780
; Patent No. 5459250
; GENERAL INFORMATION:
; APPLICANT: CLAUDIO BASILICO
; APPLICANT: DANIELA TALARICO
; TITLE OF INVENTION: MAMMALIAN GROWTH FACTOR
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Darby & Darby P.C.
; STREET: 805 Third Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch,
; MEDIUM TYPE: 360 Kb storage
; COMPUTER: IBM or IBM-compatible
; OPERATING SYSTEM: PC/MS-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/187,780
; FILING DATE: January 25, 1994
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/901,705
; FILING DATE: June 22, 1992
; APPLICATION NUMBER: 07/806,771
; FILING DATE: December 6, 1991
; APPLICATION NUMBER: 07/177,506
; FILING DATE: April 4, 1988
; APPLICATION NUMBER: 07/062,925
; FILING DATE: June 16, 1987
; ATTORNEY/AGENT INFORMATION:
; NAME: Howard M. Frankfort
; REGISTRATION NUMBER: 32,613
; REFERENCE/DOCKET NUMBER: 5986/13586-US3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 527-7700
; TELEFAX: (212) 753-6237
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 423
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Genomic DNA
; DESCRIPTION: found on page 5, lines 3-13, in the
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY:
; LOCATION:
; IDENTIFICATION METHOD:
; OTHER INFORMATION: This sequence can be
; OTHER INFORMATION: application, as filed.
; PUBLICATION INFORMATION:
; AUTHORS:
; TITLE:
; JOURNAL:
; VOLUME:
; ISSUE:
; PAGES:
; DATE:
; DOCUMENT NUMBER:
; FILING DATE:
; PUBLICATION DATE:
; RELEVANT RESIDUES IN SEQ ID NO: 1-423
US-08-187-780-2
Query Match 5.1%; Score 32.8; DB 1; Length 423;
Best Local Similarity 48.4%; Pred. No. 1.5;
Matches 122; Conservative 0; Mismatches 127; Indels 3; Gaps 1;
QY 162 cgaccaagacactgaagccacctggagatcagggagatggaacagtggtaggcgcagc 221
Db 66 CAACGTGGGCATCGGCTTCCACCTCCAGCGCTCCCGACGCGCATCGGCGGCGCA 125
QY 222 acaccgcagtcacgaagctcctctgagctcaaacgcttgaagccaggggtcattcaaat 281
Db 126 CGCGACACCCCGCAGCGCTCTCGAGCTCTCGCCCTGGAGCGGCGGTGGTGGCAT 185
QY 282 cctgggtgtcaagcctctctaggtttcttgcacagccagatggagctctctatggatc 341
Db 186 CTTGCGGTGGCCAGCCGCTTCTCGTGGCCATGAGCAGCAAGGCGCAAGCTCTATGGCTC 245
QY 342 gctcactttgatcctgagcctgagccttcagagaaactgctgtg99agcggttacaac 401
Db 246 GCC---CTTCTTACCAGATGATGTCACGTTCAAGGAGATTCTCTTCCCAACAACATAAA 302
QY 402 tgtgtaccagtc 413
Db 303 CGCCTACGAGTC 314
RESULT 14
US-08-187-780-5
; Sequence 5, Application US/08187780
; Patent No. 5459250
; GENERAL INFORMATION:
; APPLICANT: CLAUDIO BASILICO
; APPLICANT: DANIELA TALARICO
; TITLE OF INVENTION: MAMMALIAN GROWTH FACTOR
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Darby & Darby P.C.
; STREET: 805 Third Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM: Diskette, 5.25 inch,
; MEDIUM TYPE: 360 Kb storage
; COMPUTER: IBM or IBM-compatible
; OPERATING SYSTEM: PC/MS-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/187,780
; FILING DATE: January 25, 1994
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/901,705
; FILING DATE: June 22, 1992
; APPLICATION NUMBER: 07/806,771
; FILING DATE: December 6, 1991
; APPLICATION NUMBER: 07/177,506
; FILING DATE: April 4, 1988
; APPLICATION NUMBER: 07/062,925
; FILING DATE: June 16, 1987
; ATTORNEY/AGENT INFORMATION:
; NAME: Howard M. Frankfort
; REGISTRATION NUMBER: 32,613
; REFERENCE/DOCKET NUMBER: 5986/13586-US3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 527-7700
; TELEFAX: (212) 753-6237
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 423
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Genomic DNA
; DESCRIPTION: found on page 5, lines 3-13, in the
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY:
; LOCATION:
; IDENTIFICATION METHOD:
; OTHER INFORMATION: This sequence can be
; OTHER INFORMATION: application, as filed.
; PUBLICATION INFORMATION:
; AUTHORS:
; TITLE:
; JOURNAL:
; VOLUME:
; ISSUE:
; PAGES:
; DATE:
; DOCUMENT NUMBER:
; FILING DATE:
; PUBLICATION DATE:
; RELEVANT RESIDUES IN SEQ ID NO: 1-423
US-08-187-780-2

[illegible]

```

Db      246 GCC---CTTCTCACCAGTGACGTTCAAGGAGATTCTCTCCCAACAACACTACA   302
Qy      402 tgttaccagtc 413
Db      303 CGCCTACGAGTC 314

RESULT 15
US-08-478-485-2
; Sequence 2, Application US/08478485
; Patent No. 5883071
; GENERAL INFORMATION:
; APPLICANT: CLAUDIO BASILICO
; APPLICANT: DANIELA TALARICO
; TITLE OF INVENTION: MAMMALIAN GROWTH FACTOR
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Darby & Darby P.C.
; STREET: 805 Third Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Diskette, 3+ inch,
; MEDIUM TYPE: 1.44 MB storage
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC/MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; FILING DATE: Concurrently Herewith
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/187,780
; FILING DATE: January 25, 1994
; APPLICATION NUMBER: 07/901,705
; FILING DATE: June 22, 1992
; APPLICATION NUMBER: 07/806,771
; FILING DATE: December 6, 1991
; APPLICATION NUMBER: 07/177,506
; FILING DATE: April 4, 1988
; APPLICATION NUMBER: 07/062,925
; FILING DATE: June 16, 1987
; ATTORNEY/AGENT INFORMATION:
; NAME: Joseph R. Robinson
; REGISTRATION NUMBER: 33,448
; REFERENCE/DOCKET NUMBER: 5986/13586-US6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 527-7700
; TELEFAX: (212) 753-6237
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 423
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE:
; DESCRIPTION: Genomic DNA
; HYPOTHETICAL: No
; ANTI-SENSE: No
; FEATURE:
; NAME/KEY:
; LOCATION:
; IDENTIFICATION METHOD:
; OTHER INFORMATION: This sequence can be
; OTHER INFORMATION: found on page 5, lines 3-13, in the
; OTHER INFORMATION: application, as filed.
; PUBLICATION INFORMATION:
; AUTHORS:
; TITLE:
; JOURNAL:

```

VOLUME:

ISSUE:

PAGES:

DATE:

DOCUMENT NUMBER:

FILING DATE:

PUBLICATION DATE:

RELEVANT RESIDUES IN SEQ ID NO: 1-423

US-08-478-485-2

Query Match		5.18; Score 32.8; DB 2; Length 423;
Best Local Similarity		48.4%; Pred. No. 1.5;
Matches 122; Conservative		0; Mismatches 127; Indels 3; Gaps 1;
QY	162	cgaccaagacactaaagccacctggagatcaggaggatggaacagtggtaggcgcagc 221
Db	66	CAACGTGGGCATCGCTTCCACCTCCAGCGCTCCCGGACGCGCATCGCGGCGCGCA 125
QY	222	acaccgcagtcacgaagtctctctggagctcaaaagccttgaagccaggggtcattcaaat 281
Db	126	CGCGGACACCCGCGACAGCCTGCTGGAGCTCTCGCCCGTGGAGCGGGGCGTGGTGAGCAT 185
QY	282	cctgggtgtcaaaagcctctaggtttcttcttgccaacagccagatggagctctctatgcatc 341
Db	186	CTTCGGCGGTGGCCAGCCGGTTCTTCGTGGCCATGAGCAGCAAGGGCAAGCTCTATGGCTC 245
QY	342	gcctcactttgatcctgagcctgcagcttcagagaaactgctgtaggagcggttataaa 401
Db	246	GCC---CTCTTCACCGATGAGTGACGCTTCAAGGAGATTCTCCTTCCCAACAACACTACAA 302
QY	402	tgtgtaccagtc 413
Db	303	CGCCTACGAGTC 314

Search completed: August 6, 2001, 22:28:15
Job time: 4871 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 6, 2001, 22:30:48 ; Search time 163 Seconds
(without alignments)
2500.050 Million cell updates/sec

Title: US-09-391-861-3

Perfect score: 649

Sequence: 1 atggaatgatgatgatctag.....ctgactcttctctgaatcta 649

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 730101 seqs, 313950809 residues

Total number of hits satisfying chosen parameters: 1460202

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

N_Geneseq_0601.*
1: /SIDS8/gcgdata/geneseq/geneseq/NA1980.DAT.*
2: /SIDS8/gcgdata/geneseq/geneseq/NA1981.DAT.*
3: /SIDS8/gcgdata/geneseq/geneseq/NA1982.DAT.*
4: /SIDS8/gcgdata/geneseq/geneseq/NA1983.DAT.*
5: /SIDS8/gcgdata/geneseq/geneseq/NA1984.DAT.*
6: /SIDS8/gcgdata/geneseq/geneseq/NA1985.DAT.*
7: /SIDS8/gcgdata/geneseq/geneseq/NA1986.DAT.*
8: /SIDS8/gcgdata/geneseq/geneseq/NA1987.DAT.*
9: /SIDS8/gcgdata/geneseq/geneseq/NA1988.DAT.*
10: /SIDS8/gcgdata/geneseq/geneseq/NA1989.DAT.*
11: /SIDS8/gcgdata/geneseq/geneseq/NA1990.DAT.*
12: /SIDS8/gcgdata/geneseq/geneseq/NA1991.DAT.*
13: /SIDS8/gcgdata/geneseq/geneseq/NA1992.DAT.*
14: /SIDS8/gcgdata/geneseq/geneseq/NA1993.DAT.*
15: /SIDS8/gcgdata/geneseq/geneseq/NA1994.DAT.*
16: /SIDS8/gcgdata/geneseq/geneseq/NA1995.DAT.*
17: /SIDS8/gcgdata/geneseq/geneseq/NA1996.DAT.*
18: /SIDS8/gcgdata/geneseq/geneseq/NA1997.DAT.*
19: /SIDS8/gcgdata/geneseq/geneseq/NA1998.DAT.*
20: /SIDS8/gcgdata/geneseq/geneseq/NA1999.DAT.*
21: /SIDS8/gcgdata/geneseq/geneseq/NA2000.DAT.*
22: /SIDS8/gcgdata/geneseq/geneseq/NA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	638.4	98.4	659	21	AAAF75631 Nucleotide sequenc
2	283.8	43.7	514	22	AAF76715 Human fibroblast g
3	68.4	10.5	996	22	AAF44266 Human PRO9828 nucl
4	54.2	8.4	2133	20	AAAX52224 Protein PRO533 cdn
5	54.2	8.4	2133	20	AAAX28430 FGF homologue PRO5
6	54.2	8.4	2137	20	AAV72455 Human PRO533 cdNA.
7	54.2	8.4	2137	21	AAAC58599 Human PRO533 prote
8	54.2	8.4	2137	21	AAA30028 Human PRO533 nucle
9	54.2	8.4	2137	22	AAF58498 PRO533 coding sequ
10	54.2	8.4	2137	22	AAC87022 Nucleotide sequenc
11	54.2	8.4	2137	22	AAF72382 Human PRO533 cdNA.

12	48.2	7.4	1973	21	AAAC61159 Human fibroblast g
13	48.2	7.4	2749	21	AAAC61157 Human fibroblast g
14	44.2	6.8	534	21	AAAC61160 Human fibroblast g
15	44.2	6.8	537	21	AAAC61158 Human fibroblast g
16	44	6.8	531	21	AAAC61156 Monkey fibroblast
17	44	6.8	805	21	AAAC61155 Monkey fibroblast
18	43.8	6.7	1824	20	AAV72463 Human FGF-15 DNA f
19	40.2	6.2	627	15	AAQ58992 Diospyros texana a
20	40.2	6.2	693	15	AAQ58991 Diospyros texana a
21	37.8	5.8	2426	9	AAH80751 Sense strand of Ap
22	37	5.7	3401	7	AAH60518 Open reading frame
23	35.8	5.5	679	21	AAAF13170 Aspergillus oryzae
24	35.4	5.5	324	9	AAH81555 EPO 125 encoding e
25	35.4	5.5	582	21	AAAC46697 DNA encoding a hum
26	35.4	5.5	585	22	AAAC66882 Chimpanzee erythro
27	35.4	5.5	606	21	AAAO7253 Human EPO cDNA seq
28	35.4	5.5	616	20	AAH77361 Polynucleotide seq
29	35.4	5.5	616	21	AAH90393 DN encoding synthe
30	35.4	5.5	724	9	AAH81554 EPO 140B encoding
31	35.4	5.5	788	17	AAAT31529 Human erythropoiet
32	35.4	5.5	788	21	AAZ31999 Human EPO long cdn
33	35.4	5.5	823	18	AAAT64847 Human erythropoiet
34	35.4	5.5	1015	13	AAQ24282 Epo:IL-3 short, re
35	35.4	5.5	1072	13	AAQ24285 Epo:IL-3 Flex, rec
36	35.4	5.5	1158	20	AAH25701 Human erythropoiet
37	35.4	5.5	1245	8	AAH70360 Sequence encoding
38	35.4	5.5	1255	7	AAH60519 cDNA of clone lamb
39	35.4	5.5	1342	7	AAH60513 Erythropoietin gen
40	35.4	5.5	1583	18	AAAT62367 Erythropoietin gen
41	35.4	5.5	1585	18	AAAT62365 Erythropoietin gen
42	35.4	5.5	1586	18	AAAT62368 Erythropoietin gen
43	35.4	5.5	1587	18	AAAT62368 Erythropoietin gen
44	35.4	5.5	1789	16	AAQ92296 Erythropoietin cdn
45	35.4	5.5	2164	21	AAA46510 DNA encoding human

ALIGNMENTS

RESULT 1

AAAF75631
ID AAA75631 standard; DNA; 659 BP.

XX AC AAA75631;

XX AC AAA75631;

DT 22-JAN-2001 (first entry)

XX DE Nucleotide sequence of murine fibroblast growth factor (FGF)-21.

XX KW pd10-VEGFuc; gene delivery vector; eye disease; neovascular disease;
KW neurotrophic factor; anti-angiogenic factor; eye disease; glaucoma;
KW macular degeneration; diabetic retinopathy; retinitis pigmentosa;
KW inherited retinal degeneration; surgery-induced retinopathy;
KW retinal detachment; photic retinopathy; toxic retinopathy;
KW trauma-induced retinopathy; wet age related macular degeneration;
KW ARMD; retinopathy; fibroblast growth factor-20; FGF-20; ss.

XX OS Mus sp.

XX FH Key Location/Qualifiers

XX CDS 14..646

XX FT /*tag= a

XX FT /product= "Fibroblast growth factor 21"

XX PN WO200054813-A2.

XX XX 21-SEP-2000.

XX XX 15-MAR-2000; 2000WO-US07062.

XX XX 15-MAR-1999; 99US-0124460.

XX PR 06-JAN-2000; 2000US-0174984.

XX XX


```

Db 221 cagaagccacctggagatcaggagatggacggtggggcgctgctgaccagagcc 280
QY 233 cagaagctctcctggagctcaagcccttaagccaggggtcattcaaatcctgggtgca 292
Db 281 cgaagagctctcctggagctcgaagcccttgaaagccggaggtattcaaatcctggagtgca 340
QY 293 aagcctctaggtttctttgccaacagccagatggagctctctatgagtcgctcactttg 352
Db 341 agacatccaggttctctgcccagcggccagatggggcctgatgatgctccactttg 400
QY 353 atctagagcctgcagctcagagaactctgctgtaggagacgggttacatgtgtaccagt 412
Db 401 accctgagcctgcagctccggagctgcttcttgagcagcgatcaaatgtttaccagt 460
QY 413 ctgaagcccatggcctgcccctgcgtctgcc 443
Db 461 cgaagcccccacggcctcccgctgcacttgcc 491

RESULT 3
AAF44266
ID AAF44266 standard; cDNA; 996 BP.
XX
AC AAF44266;
XX
DT 02-APR-2001 (first entry)
XX
DE Human PRO9828 nucleotide sequence SEQ ID NO:510.
XX
KW Human; secreted and transmembrane protein; PRO; cytotstatic;
KW cell death; cancer; chromosomal mapping; gene mapping; tissue typing;
KW diagnostic assay; ss.
OS Homo sapiens.
XX
PN WO200073454-A1.
XX
PD 07-DEC-2000.
XX
PF 30-MAR-2000; 2000WO-US08439.
XX
PR 02-JUN-1999; 99WO-US12252.
PR 23-JUN-1999; 99US-0141037.
PR 07-JUL-1999; 99US-0143048.
PR 20-JUL-1999; 99US-0144758.
PR 26-JUL-1999; 99US-0145698.
PR 28-JUL-1999; 99US-0146222.
PR 17-AUG-1999; 99US-0149396.
PR 15-SEP-1999; 99WO-US21090.
PR 15-SEP-1999; 99WO-US21547.
PR 08-OCT-1999; 99US-0158663.
PR 30-NOV-1999; 99WO-US28313.
PR 01-DEC-1999; 99WO-US28301.
PR 16-DEC-1999; 99WO-US30095.
PR 20-DEC-1999; 99WO-US30911.
PR 05-JAN-2000; 2000WO-US00219.
PR 06-JAN-2000; 2000WO-US00376.
PR 11-FEB-2000; 2000WO-US03565.
PR 18-FEB-2000; 2000WO-US04341.
PR 22-FEB-2000; 2000WO-US04414.
PR 24-FEB-2000; 2000WO-US04914.
PR 24-FEB-2000; 2000WO-US05004.
PR 02-MAR-2000; 2000WO-US05841.
PR 15-MAR-2000; 2000WO-US06884.
PR 20-MAR-2000; 2000WO-US07377.
XX
PA (GETH ) GENENTECH INC.
XX
PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
PI Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi CJ, Gurney AL, Kijavini IJ, Napier MA, Pan J, Paoni NF;
PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;

```

```

PI Zhang Z;
XX
XX WPI: 2001-032160/04.
DR P-PSDB; AAB65297.
XX
PT PRO polynucleotides used to produce polypeptides used to target
PT bioactive molecules such as toxins, radiolabels or antibodies, to
PT specific cells, to cause targeted cell death -
XX
XX Claim 2; Fig 323; 935pp; English.
XX
CC The present invention describes human secreted and transmembrane PRO
CC proteins. The PRO proteins have cytostatic activity. The PRO proteins
CC can be used for targeted delivery of bioactive molecules, such as
CC toxins, radiolabels or antibodies, that cause cell death. PRO nucleotide
CC sequences, and their fragments, can be used as hybridisation probes, in
CC chromosomal and gene mapping, and in the generation of anti-sense RNA
CC and DNA. They may also be used to produce transgenic animals which are
CC nucleotide and protein sequence can be used for tissue typing and in
CC treating cancer. Anti-PRO antibodies can be used in diagnostic assays.
CC AAF44270 to AAF44470 represent PCR primers and hybridisation probes used
CC in the isolation of human PRO sequences. AAF4087 to AAF44269 and
CC AAB65154 to AAB65300 represent human PRO polynucleotide and protein
CC sequences given in the exemplification of the present invention.
XX
SQ Sequence 996 BP; 222 A; 320 C; 260 G; 194 T; 0 other;

Query Match 10.5%; Score 68.4; DB 22; Length 996;
Best Local Similarity 53.8%; Pred. No. 1.9e-09;
Matches 141; Conservative 0; Mismatches 121; Indels 0; Gaps 0;

QY 180 ccactggagatcaggagagatggaacagtggttaggcgcagcacacccagtcagaaag 239
Db 384 ccactgcagatccacaagaatggcatgtggtggtgcgcacccatcctctacag 443
QY 240 tctcctggagctcaaaagccttgaaagccagggttcattcaaatcctggtgtcaagcctc 299
Db 444 tgcctgatgatcagatcagagagatgctgcttgggtgattacaggtgtgatgagcag 503
QY 300 taggtttctttggccacagccagatggagctctctatggtgcctcactttgactctga 359
Db 504 aagatcctctgcatgatttcagaggcaacatttttggatcacactatttcgaccgga 563
QY 360 ggcctgcagcttcagaaactgctgctggagacggttacaaatgtgtaccagttgaagc 419
Db 564 gaactgcaggttccacaccagacgctggaaacgggtacgaogtctaccactctctca 623
QY 420 ccattggcctgcccctgcgtctg 441
Db 624 gataccttctcgtgctgctg 645

RESULT 4
AA552224
ID AAX52224 standard; DNA; 2133 BP.
XX
AC AAX52224;
XX
XX 25-JUN-1999 (first entry)
XX
DE Protein PRO533 cDNA clone DNA49435-1219.
XX
KW Secreted protein; transmembrane protein; human; enterocolitis;
KW Zollinger-Ellison syndrome; gastrointestinal ulceration;
KW congenital microvillus atrophy; skin disease; cell growth;
KW abnormal keratinocyte differentiation; psoriasis; epithelial cancer;
KW Parkinson's disease; Alzheimer's disease; ALS; neuropathy;
KW fibromodulin; dermal scarring; Usher Syndrome; Atrophila areata;
KW anti-thrombotic; wound healing; tissue repair; ss.
XX
OS Homo sapiens.

```


PT useful for diagnosing and treating cancers -

XX Claim 50; Fig 3; 196pp; English.

XX The present invention relates to PRO proteins and coding sequences. The
CC present sequence is the coding sequence for one such PRO protein.
CC It was found that the PRO genes are amplified in the genome of tumour
CC cells. The gene amplification is expected to be associated with the
CC overexpression of the gene product and contributes to tumorigenesis.
CC Therefore, antagonists of PRO proteins are useful for the treatment of
CC benign or malignant tumours, leukemias, lymphoid malignancies and other
CC disorders such as neuronal, glial, astrocytal, hypothalamic, glandular,
CC epithelial, inflammatory and immunologic disorders.

XX Sequence 2137 BP; 422 A; 648 C; 598 G; 469 T; 0 other;

Query Match 8.4%; Score 54.2; DB 22; Length 2137;
Best Local Similarity 48.3%; Pred. NO. 2e-05;
Matches 183; Conservative 0; Mismatches 193; Indels 3; Gaps 1;

QY 66 cctgctgggggtctaccaagcataccatccctgaactccagccccctccctccagtttgg 125
DB 520 cgtgcccgggcccctctcgttcggaagcggggcccccacgtgcactacggctgggg 579
QY 126 ggttaagtcggcagaggtacctctacacagatgacgacccaag---acactgaagccca 182
DB 580 cgaccccatccgctcgccgacgtgtacacctccgccccacgggtctccagctggt 639
QY 183 cctgagatcagggaggtggaacagtggttaggcgcagcacaccagtcacgaaagtct 242
DB 640 cctgcgcatccgtgcgacgctgtgtagtgcgctggggggcgagcgcgacagttt 699
QY 243 cctgagctcaagccttgaagccgggtcattcaaatcctgggtgtcaagcctctag 302
DB 700 gctggagatcaaggcagctcgtctgcgacgggcccacatcaaggcgcgacagcgtgcg 759
QY 303 gttctttgccaacagcagatggagctctctatgctcgtccacttctgactcctggagc 362
DB 760 gtacctctgcatggggcgccgacgcaagatcaggggcttccagtccggaggaaga 819
QY 363 ctgcagcttcaagaaactgctgtgagagcaggttacaatgtgtaccagtgtaagccca 422
DB 820 cttgtgtcttcggaggagagatccgcccagatggtacaaatgtgtaccgacgagaagca 879
QY 423 tggcctgcccctgcgtctg 441
DB 880 ccgctcccggtctccctg 898

RESULT 10
AAC87022
ID AAC87022 standard; cDNA; 2137 BP.

XX AAC87022;

XX 20-APR-2001 (first entry)

DE Nucleotide sequence of human polypeptide PRO533.

XX Human; secreted protein; transmembrane protein; PRO196; PRO444; PRO183;
KW PRO185; PRO210; PRO215; PRO217; PRO242; PRO288; PRO365; PRO1361; PRO1308;
KW PRO1183; PRO1272; PRO1419; PRO4999; PRO7170; PRO248; PRO353; PRO1318;
KW PRO1600; PRO9940; PRO533; PRO301; PRO187; PRO337; PRO1411; PRO4356;
KW PRO246; PRO265; PRO941; PRO10096; PRO6003; PRO6004; PRO350; PRO2630;
KW PRO6309; cell death; genetic disorder; transgenic animal; gene therapy;
ss.

OS Homo sapiens.

XX Key Location/Qualifiers

PH CDS 464..1114

FT /*tag= a

FT sig_peptide 464..529
XX /*tag= b
XX WO200077037-A2.

XX 21-DEC-2000.

XX 22-MAY-2000; 2000WO-US14042.

XX 15-JUN-1999; 99US-0139695.

XX 20-JUL-1999; 99US-0145070.

XX 26-JUL-1999; 99US-0145698.

XX 17-AUG-1999; 99US-0149396.

XX 01-SEP-1999; 99WO-US20111.

XX 08-SEP-1999; 99WO-US20594.

XX 15-SEP-1999; 99WO-US21090.

XX 15-SEP-1999; 99WO-US21547.

XX 30-NOV-1999; 99WO-US28313.

XX 01-DEC-1999; 99WO-US28301.

XX 02-DEC-1999; 99WO-US28565.

XX 07-DEC-1999; 99US-0169495.

XX 05-JAN-2000; 2000WO-US00219.

XX 18-FEB-2000; 2000WO-US04341.

XX 22-FEB-2000; 2000WO-US04342.

XX 01-MAR-2000; 2000WO-US04414.

XX 02-MAR-2000; 2000WO-US05601.

XX 20-MAR-2000; 2000WO-US05841.

XX 30-MAR-2000; 2000WO-US07377.

XX 15-MAY-2000; 2000WO-US08439.

XX 17-MAY-2000; 2000WO-US13358.

XX (GETH) GENENTECH INC.

XX Ashkenazi AJ, Baker KP, Botstein DA, Desnoyers L, Eaton DL;

XX Ferrara N, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;

XX Godowski PJ, Gurney AL, Kijavini IJ, Mather JP, Napier MA, Pan J;

XX Paoni NF, Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM;

XX Wood WI, Zhang Z;

XX WPI; 2001-050091/06.

XX P-PSDB; AAB31201.

XX Isolated nucleic acid molecule encoding a PRO polypeptide which is a

XX transmembrane polypeptide is useful for gene therapy and identification

XX of related polypeptides -

XX Claim 2; Fig 45; 244pp; English.

XX The present sequence encodes a human secreted and transmembrane

XX polypeptide. The specification describes human polypeptides, designated

XX PRO196, PRO444, PRO183, PRO185, PRO210, PRO215, PRO217, PRO242, PRO288,

XX PRO365, PRO1361, PRO1308, PRO1183, PRO1272, PRO1419, PRO4999, PRO7170,

XX PRO248, PRO353, PRO1318, PRO1600, PRO9940, PRO533, PRO301, PRO187,

XX PRO337, PRO1411, PRO4356, PRO246, PRO265, PRO941, PRO10096, PRO6003,

XX PRO6004, PRO350, PRO2630 and PRO6309. The biological activity of cells

XX can be modulated with agents that bind to these polypeptides, resulting

XX in the death of the cells. The polynucleotides encoding these

XX polypeptides are useful in the recombinant production of the

XX polypeptides, as a hybridisation probe to screen libraries to isolate

XX homologous sequences, or to map the gene. They may also be used for

XX analysing genetic disorders, and to produce transgenic animals which are

XX useful for the development and screening of therapeutically useful

XX reagents. The polynucleotides can also be used in gene therapy e.g. to

XX replace a defective gene.

XX Sequence 2137 BP; 422 A; 648 C; 598 G; 469 T; 0 other;

Query Match 8.4%; Score 54.2; DB 22; Length 2137;

Best Local Similarity 48.3%; Pred. No. 2e-05;

Matches 183; Conservative 0; Mismatches 193; Indels 3; Gaps 1;

Fibroblast growth factor-20; FGF-20; cytotatic; neurotropic; metastasis; neuroprotective; antiparkinsonian; anticonvulsant; hepatotropic; cancer; leukaemia; tumour angiogenesis; skeletal dysplasia; Alzheimer's disease; neurodegenerative disorder; Parkinson's disease; multiple sclerosis; amyotrophic lateral sclerosis; progressive supranuclear palsy; epilepsy; Creutzfeldt-Jakob disease; hepatic disorder; cardiovascular disorder; haematopoietic disorder; myeloproliferative disorder; human; ss.

Homo sapiens.

OS XX

XX XX

PN XX

XX XX

PD XX

XX XX

PF XX

XX XX

PR XX

XX XX

PO XX

XX XX

PI XX

XX XX

DR XX

XX XX

PT XX

XX XX

PT XX

XX XX

PT XX

XX XX

PS XX

XX XX

CC XX

XX XX

CC XX

XX XX

CC XX

XX XX

CC XX

XX XX

CC XX

XX XX

CC XX

XX XX

CC XX

XX XX

CC XX

XX XX

CC XX

XX XX

CC XX

XX XX

CC XX

XX XX

CC XX

XX XX

CC XX

XX XX

CC XX

XX XX

CC XX

XX XX

CC XX

XX XX

CC XX

XX XX

CC XX

XX XX

CC XX

XX XX

CC XX

XX XX

CC XX

XX XX

Fibroblast growth factor-20; FGF-20; cytotatic; neurotropic; metastasis; neuroprotective; antiparkinsonian; anticonvulsant; hepatotropic; cancer; leukaemia; tumour angiogenesis; skeletal dysplasia; Alzheimer's disease; neurodegenerative disorder; Parkinson's disease; multiple sclerosis; amyotrophic lateral sclerosis; progressive supranuclear palsy; epilepsy; Creutzfeldt-Jakob disease; hepatic disorder; cardiovascular disorder; haematopoietic disorder; myeloproliferative disorder; human; ss.

Homo sapiens.

OS XX

XX XX

PN XX

XX XX

PD XX

XX XX

PF XX

XX XX

PR XX

XX XX

PO XX

XX XX

PI XX

XX XX

DR XX

XX XX

PT XX

XX XX

PT XX

XX XX

PT XX

XX XX

PS XX

XX XX

CC XX

XX XX

CC XX

XX XX

CC XX

XX XX

CC XX

XX XX

CC XX

XX XX

CC XX

XX XX

CC XX

XX XX

CC XX

XX XX

CC XX

XX XX

CC XX

XX XX

CC XX

XX XX

CC XX

XX XX

CC XX

XX XX

CC XX

XX XX

CC XX

XX XX

CC XX

XX XX

CC XX

XX XX

CC XX

XX XX

CC XX

XX XX

CC XX

XX XX

CC XX

XX XX

Fibroblast growth factor-20; FGF-20; cytotatic; neurotropic; metastasis; neuroprotective; antiparkinsonian; anticonvulsant; hepatotropic; cancer; leukaemia; tumour angiogenesis; skeletal dysplasia; Alzheimer's disease; neurodegenerative disorder; Parkinson's disease; multiple sclerosis; amyotrophic lateral sclerosis; progressive supranuclear palsy; epilepsy; Creutzfeldt-Jakob disease; hepatic disorder; cardiovascular disorder; haematopoietic disorder; myeloproliferative disorder; human; ss.

Homo sapiens.

OS XX

XX XX

PN XX

XX XX

PD XX

XX XX

PF XX

XX XX

PR XX

XX XX

PO XX

XX XX

PI XX

XX XX

DR XX

XX XX

PT XX

XX XX

PT XX

XX XX

PT XX

XX XX

PS XX

XX XX

CC XX

XX XX

CC XX

XX XX

CC XX

XX XX

CC XX

XX XX

CC XX

XX XX

CC XX

XX XX

CC XX

XX XX

CC XX

XX XX

CC XX

XX XX

CC XX

XX XX

CC XX

XX XX

CC XX

Sequence 1973 BP; 580 A; 463 C; 505 G; 425 T; 0 other;

Query Match 7.4%; Score 48.2; DB 21; Length 1973;

Best Local Similarity 52.2%; Pred. No. 0.00085;

Matches 107; Conservative 0; Mismatches 98; Indels 0; Gaps 0;

QY 237 agtctctggagctcaagccttgagccaggggtcattcaaatcctgggtgtcaaacg 296

DB 1061 aggtgcccctgatgcagatcagagagatgctggtgtgtgattacaggtgtgatgag 1120

QY 297 cttcaggtttcttgcacacagcagatggagctctctatgagctcacttgatcc 356

DB 1121 cagagatcactctgtcattggtttcagagggcaacatttttgatcacactatttcgaccc 1180

QY 357 tgagccctgcagcttcagagactgctgtgaggaacggttacaatgtgtaccagtctga 416

DB 1181 ggagactgcaggtttccacacacagacgctgtgaaacgggttaacgcttaccactctcc 1240

QY 417 agcccatggcctgcctctgctgtcgt 441

DB 1241 teagtataccttctcgttcagctctg 1265

RESULT 13

AAC61157

ID AAC61157 standard; cDNA; 2749 BP.

XX AC AAC61157;

XX AC AAC61157;

DT 07-FEB-2001 (first entry)

XX XX

XX XX

DE Human fibroblast growth factor-20 (FGF-20) cDNA sequence.

XX XX

XX XX

KW Fibroblast growth factor-20; FGF-20; cytotatic; neurotropic; metastasis;

KW neuroprotective; antiparkinsonian; anticonvulsant; hepatotropic; cancer;

KW leukaemia; tumour angiogenesis; skeletal dysplasia; Alzheimer's disease;

KW neurodegenerative disorder; Parkinson's disease; multiple sclerosis;

KW amyotrophic lateral sclerosis; progressive supranuclear palsy; epilepsy;

KW Creutzfeldt-Jakob disease; hepatic disorder; cardiovascular disorder;

KW haematopoietic disorder; myeloproliferative disorder; human; ss.

XX XX

OS Homo sapiens.

XX XX

PN WO200060085-A1.

XX XX

PD 12-OCT-2000.

XX XX

PF 27-MAR-2000; 2000WO-US08076.

XX XX

PR 02-APR-1999; 99US-0127534.

XX XX

PR 03-DEC-1999; 99US-0454470.

XX XX

XX (MILL-) MILLENNIUM PHARM INC.

XX XX

XX XX

PI Curtis RAJ, Wrighton NC;

XX XX

DR WPI; 2000-647346/62.

XX XX

DR P-PSDB; AAY85638.

XX XX

XX Novel nucleic acids encoding fibroblast growth factor-20, useful for

CC detecting and modulating FGF-20 and for treating, e.g. cancer,

CC neurodegenerative disorders, hepatic disorders and cardiovascular

CC disorders -

PT Claim 1; Fig 9; 149pp; English.

XX XX

XX Polynucleotide sequences AAC61155-C61160 encode fibroblast growth

CC factor-20 (FGF-20) proteins AAY85637-Y85639. The invention includes

CC FGF-20 sequences isolated from humans and monkeys. Proteins,

CC polynucleotides, agonists and antagonists of the invention have

CC cytotatic; neurotropic; neuroprotective; antiparkinsonian; anticonvulsant

CC and hepatotropic activity. The peptides, nucleotides and their binding

CC agents may be used to modulate the expression or activity of FGF-20, or to

CC diagnose aberrant FGF-20 expression. FGF20 activity or expression may be

CC down-regulated to treat proliferative or differentiative disorders (e.g.

CC cancers and leukaemia), tumour angiogenesis and metastasis, skeletal

CC dysplasia, neurodegenerative disorders (e.g. Alzheimer's disease,

CC Parkinson's disease, multiple sclerosis, amyotrophic lateral sclerosis,

CC progressive supranuclear palsy, epilepsy or Creutzfeldt-Jakob disease),

CC hepatic disorders, cardiovascular disorders and haematopoietic and/or

CC myeloproliferative disorders.

XX XX

XX Sequence 2749 BP; 747 A; 645 C; 633 G; 724 T; 0 other;

QY 237 agtctctggagctcaagccttgagccaggggtcattcaaatcctgggtgtcaaacg 296

DB 316 aggtgcccctgatgcagatcagagagatgctggtgtgtgattacaggtgtgatgag 375

QY 297 cttcaggtttcttgcacacagcagatggagctctctatgagctcacttgatcc 356

DB 376 cagagatcactctgctgatttcagagggcaacatttttgatcacactatttcgaccc 435

Query Match 7.4%; Score 48.2; DB 21; Length 2749;

Best Local Similarity 52.2%; Pred. No. 0.00096;

Matches 107; Conservative 0; Mismatches 98; Indels 0; Gaps 0;

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 6, 2001, 21:09:08 ; Search time 114.92 Seconds
(without alignments)
241.769 Million cell updates/sec

Title: US-09-391-861-4
Perfect score: 1115
Sequence: 1 MEWRSRVGTGLWVRLLLA.....SSDPLSMVEPLQGRSPSYAS 210

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 425026 seqs, 132305027 residues

Total number of hits satisfying chosen parameters: 425026

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: SPREMBL16.*
- 2: sp_archaea.*
- 3: sp_bacteria.*
- 4: sp_fungi.*
- 5: sp_human.*
- 6: sp_invertebrate.*
- 7: sp_mammal.*
- 8: sp_mhc.*
- 9: sp_organelle.*
- 10: sp_phage.*
- 11: sp_plant.*
- 12: sp_rodent.*
- 13: sp_unclassified.*
- 14: sp_vertebrate.*
- 15: sp_virus.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	1115	100.0	210	11	Q9JJN1	Q9JJN1 mus musculus
2	793.5	71.2	209	4	Q9NSA1	Q9NSA1 homo sapien
3	241	21.6	251	4	Q9GZV9	Q9GZV9 homo sapien
4	235	21.1	251	11	Q9EPC2	Q9EPC2 mus musculus
5	212.5	19.1	227	13	Q9DDN0	Q9DDN0 gallus gall
6	173.5	15.6	191	13	Q9DFC9	Q9DFC9 brachydanio
7	171	15.3	206	13	Q9YGD8	Q9YGD8 oncorhynch
8	162	14.5	196	13	Q9YH31	Q9YH31 notophthalm
9	144	12.9	194	6	P79150	P79150 canis famli
10	144	12.9	194	6	P79150	P79150 canis famli
11	142.5	12.8	170	4	Q9ESL9	Q9ESL9 mus musculus
12	141.5	12.7	212	13	Q42407	Q42407 gallus gall
13	139	12.5	162	11	Q9ESS2	Q9ESS2 mus musculus
14	139	12.5	185	11	Q9ERN5	Q9ERN5 rattus norv
15	139	12.5	211	4	Q9NP95	Q9NP95 homo sapien
16	138	12.4	194	6	Q9N198	Q9N198 sus scrofa
17	138	12.4	212	11	Q9EST9	Q9EST9 rattus norv
18	135.5	12.2	213	6	Q9N1B9	Q9N1B9 ovis aries
19	135	12.1	207	11	Q9ESL8	Q9ESL8 mus musculus

20	135	12.1	207	11	Q9ER05	Q9ER05 mus musculus
21	133	11.9	130	6	Q77767	Q77767 canis famli
22	132	11.8	196	4	P78443	P78443 homo sapien
23	131	11.7	208	13	Q9PVY1	Q9PVY1 xenopus lae
24	129	11.6	170	11	Q60487	Q60487 cavia porce
25	125	11.2	425	5	Q76831	Q76831 caenorhabdi
26	124	11.1	199	13	Q9IAI3	Q9IAI3 gallus gall
27	123	11.0	245	13	Q9W6A2	Q9W6A2 gallus gall
28	123	11.0	252	11	Q89096	Q89096 rattus norv
29	121	10.9	192	11	Q9ERW3	Q9ERW3 rattus norv
30	121	10.9	237	13	Q9IAI6	Q9IAI6 gallus gall
31	121	10.9	253	13	Q9IAI5	Q9IAI5 gallus gall
32	118.5	10.6	108	6	Q9N1S7	Q9N1S7 capreolus c
33	118	10.6	106	6	Q9N1S8	Q9N1S8 capreolus c
34	116	10.4	101	13	P79706	P79706 cynops pyrr
35	115	10.3	127	4	Q99517	Q99517 homo sapien
36	115	10.3	163	11	Q9JHL9	Q9JHL9 mus musculus
37	113.5	10.2	146	13	Q07659	Q07659 gallus gall
38	113.5	10.2	181	13	Q9IAI7	Q9IAI7 gallus gall
39	113.5	10.2	243	13	Q9W6A1	Q9W6A1 gallus gall
40	110	9.9	97	4	Q9NSJ0	Q9NSJ0 homo sapien
41	110	9.9	192	4	Q95830	Q95830 homo sapien
42	109.5	9.8	64	11	Q9JK55	Q9JK55 rattus norv
43	99.5	8.9	76	6	Q9NOV2	Q9NOV2 ovis aries
44	98.5	8.8	74	6	Q77561	Q77561 oryctolagus
45	98	8.8	770	5	P91672	P91672 drosophila

ALIGNMENTS

RESULT 1
Q9JJN1
ID Q9JJN1 PRELIMINARY; PRT; 210 AA.
AC Q9JJN1;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE FGF-21.
DE FGF-21.
GN FGF-21.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20461777; PubMed=10858549;
RA Nishimura T., Nakatake Y., Konishi M., Itoh N.;
RT "Identification of a novel FGF, FGF-21, preferentially expressed in the liver.";
RL Biochim. Biophys. Acta 1492:203-206(2000).
DR EMBL; AB025718; BAA99416.1; -;
DR InterPro; IPR002209; -;
DR InterPro; IPR002348; -;
DR Pfam; PF00167; FGF; 1.
DR PRINTS; PR00263; HBGFFGF.
DR PRINTS; PR00262; IL1HBGF.
DR SMART; SM00442; FGF; 1.
SQ SEQUENCE 210 AA; 23237 MW; AE02ABA6477E6F0 CRC64;

Query Match 100.0%; Score 1115; DB 11; Length 210;
Best Local Similarity 100.0%; Pred. No. 8.7e-96;
Matches 210; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MEWRSRVGTGLWVRLLLAVLLGVGTQAIPIPDSSPLQFGGQVQRORYLYTDDQDTEA 60
Db 1 MEWRSRVGTGLWVRLLLAVLLGVGTQAIPIPDSSPLQFGGQVQRORYLYTDDQDTEA 60
QY 61 HLEIREDTGVVGAHRSPESLLELKALPGVITQLGVKASRFLCCQPDGALYGSPPHDPDE 120
Db 61 HLEIREDTGVVGAHRSPESLLELKALPGVITQLGVKASRFLCCQPDGALYGSPPHDPDE 120

```
QY 121 ACSFRELLEDGYNVYQSAHGLPLRLPKQDSPNQDATSWGVPRLPGLLHEPDQAG 180
Db 121 ACSFRELLEDGYNVYQSAHGLPLRLPKQDSPNQDATSWGVPRLPGLLHEPDQAG 180
QY 181 FLPPEDPDVGGSDPLSMVPEPLQGRSPSYAS 210
Db 181 FLPPEDPDVGGSDPLSMVPEPLQGRSPSYAS 210

RESULT 2
Q9NSAL PRELIMINARY; PRT; 209 AA.
AC Q9NSAL;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-MAR-2001 (TReMBLrel. 16, Last annotation update)
DE FGF-21.
GN FGF-21.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20461777; PubMed=10858549;
RA Nishimura T., Nakatake Y., Konishi M., Itoh N.;
RT "Identification of a novel FGF, FGF-21, preferentially expressed in
the liver.";
RL Biochim. Biophys. Acta 1492:203-206(2000).
DR EMBL; AB021975; BAA99415.1; -.
DR InterPro; IPR002209; -.
DR Pfam; PF00167; FGF_1.
DR PRINTS; PR00263; HBGF.FGF.
DR SMART; SM00442; FGF; 1.
SQ SEQUENCE 209 AA; 22300 MW; 27925C52A0023823 CRC64;
```

```
Query Match 71.2%; Score 793.5; DB 4; Length 209;
Best Local Similarity 78.9%; Pred. No. 5.8e-66;
Matches 157; Conservative 10; Mismatches 31; Indels 1; Gaps 1;
```

```
QY 12 GLWVRLLLAVFLGLGVQAVPIPDSSPLLOFGQVQRORYLYTDDQDTEAHLEIREGTVV 71
Db 12 GLWVS-VLGLLGLGACQAHPIPDSSPLLOFGQVQRORYLYTDDQDTEAHLEIREGTVG 70
QY 72 GAAHRSPESSLELKALKPGVIQILGVKASRFLCQPDGALYGSHPDFPEACSFRELLLED 131
Db 71 GAADSPESLQLKALKPGVIQILGVKTSRFLCQPDGALYGSHPDFPEACSFRELLLED 130
QY 132 GYNVYQSEAHGLPLRLPKQDSPNQDATSWGVPRLPGLLHEPDQAGFLPPEPDVGS 191
Db 131 GYNVYQSEAHGLPLRLPKQDSPNQDATSWGVPRLPGLLHEPDQAGFLPPEPDVGS 190
QY 192 SDPLSMVPEPLQGRSPSYAS 210
Db 191 SDPLSMVPEPLQGRSPSYAS 209
```

```
RESULT 3
Q9GZV9 PRELIMINARY; PRT; 251 AA.
AC Q9GZV9;
DT 01-MAR-2001 (TReMBLrel. 16, Created)
DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TReMBLrel. 16, Last annotation update)
DE FGF-23 (FGF23).
GN FGF23.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
```

```
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=11032749;
RA Yamashita T., Yoshioka M., Itoh N.;
RT "Identification of a novel fibroblast growth factor, FGF-23,
preferentially expressed in the ventrolateral thalamic nucleus of the
brain.";
RL Biochem. Biophys. Res. Commun. 277:494-498(2000).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=20517346; PubMed=11062477;
RA White K.E., Evans W.E., O'Riordan J.L.H., Speer M.C., Econs M.J.,
RA Lorenz-Depiereux B., Grabowski M., Meitinger T., Strom T.M.;
RT "Autosomal dominant hypophosphataemic rickets is associated with
mutations in FGF23.";
RL Nat. Genet. 26:345-348(2000).
DR EMBL; AB037973; BAB13477.1; -.
DR EMBL; AF263537; AAG09917.1; -.
SQ SEQUENCE 251 AA; 27954 MW; 6093BD0CC50C2489 CRC64;
```

```
Query Match 21.6%; Score 241; DB 4; Length 251;
Best Local Similarity 32.3%; Pred. No. 1.3e-14;
Matches 71; Conservative 38; Mismatches 71; Indels 40; Gaps 8;
```

```
QY 11 LGLWVRLLLAVFLGLGVQAVPIPDSSPLLOFGQVQRORYLYTDDQDTEAHLEIREG 68
Db 6 LRLWVLCALSCVCSVLRLAY--PNASPLGSSWGGLI---HLYTATARNs-YHLQIHKG 59
QY 69 TVVGAHRSPESSLELKALKPGVIQILGVKASRFLCQPDGALYGSHPDFPEACSFRELL 128
Db 60 HVDGAPHQTIYSALMIRSEDAGFVITGVMSRRYLCMDFRGNIFGSHYFDPENCRFQHOT 119
QY 129 LEDGYNVYQS-EAHGLPLRLPKQDSPNQDATSWGVPRLPGLLHEPDQAG----- 178
Db 120 LENGVDVYHSPQYHFL-----VSLGRAKRAFLPGMNPDPYQFLSRNEIP 165
QY 179 -AGFLPPEP-----PDVGSDDLPMVPEPLQGRSPSYAS 210
Db 166 LIHFWTPPRHRSRSEDSDSERDPLNLKPRARMTAPAS 205
```

```
RESULT 4
Q9EPC2 PRELIMINARY; PRT; 251 AA.
AC Q9EPC2;
DT 01-MAR-2001 (TReMBLrel. 16, Created)
DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TReMBLrel. 16, Last annotation update)
DE FGF-23 (FGF23).
GN FGF23.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=11032749;
RA Yamashita T., Yoshioka M., Itoh N.;
RT "Identification of a novel fibroblast growth factor, FGF-23,
preferentially expressed in the ventrolateral thalamic nucleus of the
brain.";
RL Biochem. Biophys. Res. Commun. 277:494-498(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C; TISSUE=WHOLE EMBRYO;
RX MEDLINE=20517346; PubMed=11062477;
RA White K.E., Evans W.E., O'Riordan J.L.H., Speer M.C., Econs M.J.,
RA Lorenz-Depiereux B., Grabowski M., Meitinger T., Strom T.M.;
RT "Autosomal dominant hypophosphataemic rickets is associated with
mutations in FGF23.";
RL Nat. Genet. 26:345-348(2000).
DR EMBL; AB037889; BAB13478.1; -.
OX NCBI_TaxID=10090;
```



```

QY   156 DATSWGVPVRLP 167
      |           |||
Db    188 TVT-----HELP 194

RESULT 9
ID P79150 PRELIMINARY;          PRT;    194 AA.
AC Q9E150;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE KERATINOCYTE GROWTH FACTOR.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Etheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=96115;
RN NCBISeqID=150;
RS SEQUENCE FROM N.A.
RP MEDLINE=96226403; PubMed=8634153;
RX Canatan H., Chang W.Y., Sugimoto Y., Shidaifat F., Kulp S.K.,
RA Bueggemeier R.W., Lin Y.C.;
RT "Keratinocyte growth factor (KGF/GF-7) has a paracrine role in canine prostate: molecular cloning of mRNA encoding canine KGF.";
RL DNA Cell Biol. 15:247-254(1996).
DR EMBL: U08000; AAB38972.1; -.
DR HSP: P05230; 2AFG.
DR InterPro: IPR002209; -.
DR InterPro: IPR002348; -.
DR Pfam: PF00167; FGF; 1.
DR PRINTS: PR00263; HBGGFFGF.
DR PRINTS: PR00262; ILIHGFG.
DR ProDom: PD000831; -; 1.
DR PROSITE: PS00247; HBGF_FGF; 1.
DR SMART: SM00442; FGF; 1.
SQ SEQUENCE 194 AA; 22476 MW; 8B4E56304B8F14D6 CRC64;

Query Match            12.9%; Score 144; DB 6; Length 194;
Best Local Similarity 28.2%; Pred.No. 9.6e-06;
Matches 40; Conservative 29; Mismatches 47; Indels 26; Gaps

QY   42 GGVRQRILYTDDQTEAHLEIREDTGVVGAH-RSPESLLELKALKPGVIQLGVKAS 100
      || :||| |:| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db    61 GGDIVRRLEFC---RTQWYLRI DRKGKYGTQEMKNSYNIMEIRTVAVGI VAIKVGESE 116

QY   101 RFTCQQPDGALYGSHDFDEACSFRELLEDGYNNVQS-----EAHGLPLR 146
      :|| :|| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db    117 YYLAMNKEGKLAKKCN-EDCNFKELILENHNTYSAAKWTHSGGMFVALNQGVPR 175

QY   147 LPQKDSPNDATSNGPVRLPM 168
      | :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db    176 --GKTTKKEOKTA----HELPM 191

RESULT 10
ID Q9ESI9 PRELIMINARY;          PRT;    212 AA.
AC Q9ESL9;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DE FIBROBLAST GROWTH FACTOR 20.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Etheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN NCBISeqID=100;
RS SEQUENCE FROM N.A.
RP Itoh N.;
RX Submitted (SEP-2000) to the ENBL/GenBank/DDBJ databases
RL *Mus musculus mRNA for FGF-20(FGF20).";
```

```
DR EMBL; AB049218; BAB16406.1; -.
SQ SEQUENCE 212 AA; 23659 MW; 174DBCE8915B69EF CRC64;

Query Match 12.9%; Score 144; DB 11; Length 212;
Best Local Similarity 35.3%; Pred. No. 1.1e-05;
Matches 53; Conservative 12; Mismatches 65; Indels 20; Gaps 7;

QY 33 PDSSPLQFGGQVQRORYLYTDDQDTEAHLEIREDTGVVGAHRSPEL---LELKALP 89
DB 52 PGSEVLAHLHGILRRRQLYC-----RTGHLLQILPDGTVGQT--RODHSFLGILEFISVAV 105
QY 90 GVIQTLGVKASRFLLQCPDGGALYSGPHDFPEACSFRELLLEDGYNVYOSE--AHGLPLR- 146
DB 106 GLVSIKRGVDSGLYLGMDKGLYSEKLTSE-CIFREQFEENWYNTYSSNIYKHGNTGRR 164
QY 147 ----LPQKDSPNQDATSWGP---VRFLPMP 169
DB 165 YFVALNKDGTPRDGARSRRKQKFTHFLRP 194

RESULT 11
Q9HCT0 PRELIMINARY; PRT; 170 AA.
AC Q9HCT0;
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DE FGF-22.
GN FGF22.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Itoh N.;
RT "human FGF-22.";
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB012925; BAB13479.1; -.
SQ SEQUENCE 170 AA; 19662 MW; CB88918C2D54ACE7 CRC64;

Query Match 12.8%; Score 142.5; DB 4; Length 170;
Best Local Similarity 33.1%; Pred. No. 1.1e-05;
Matches 52; Conservative 24; Mismatches 66; Indels 15; Gaps 8;

QY 4 MRSRVGTGLG-LWVRLLAFLVLLGVYQAYPIPDSSPLQFGGQVQRORYLYTDDQDTEAHL 62
DB 1 MRRL-LWGLAWLLARAPDAAGTSPASRGRSYPHLE--GDVWRRLFS-----STHFFL 53
QY 63 EIREDTGVVGAHR-SPESLLELKALKPGVIOILGVKASRFLLCQPDGALYSGPHDFPEA 121
DB 54 RVDPGRGVQGTWRHGGQDSILRISRVGVVVIKAVSSGYVAMNRRGLYGRSLYTVD- 112
QY 122 CSFRELLEDGYNVYOSE---AHGLP--LRLPQKDSP 153
DB 113 CRFRERIEENGHTYASQRWRRRGQPMFLDRGGP 149

RESULT 12
O42407 PRELIMINARY; PRT; 212 AA.
AC O42407;
DT 01-JAN-1998 (Tremblrel. 05, Created)
DT 01-JUN-1998 (Tremblrel. 06, Last sequence update)
DE FTBROBLAST GROWTH FACTOR 10.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
OX NCBI_TaxID=9031;

DR EMBL; AB049218; BAB16406.1; -.
SQ SEQUENCE 212 AA; 23659 MW; 174DBCE8915B69EF CRC64;

Query Match 12.9%; Score 144; DB 11; Length 212;
Best Local Similarity 35.3%; Pred. No. 1.1e-05;
Matches 53; Conservative 12; Mismatches 65; Indels 20; Gaps 7;

QY 33 PDSSPLQFGGQVQRORYLYTDDQDTEAHLEIREDTGVVGAHRSPEL---LELKALP 89
DB 52 PGSEVLAHLHGILRRRQLYC-----RTGHLLQILPDGTVGQT--RODHSFLGILEFISVAV 105
QY 90 GVIQTLGVKASRFLLQCPDGGALYSGPHDFPEACSFRELLLEDGYNVYOSE--AHGLPLR- 146
DB 106 GLVSIKRGVDSGLYLGMDKGLYSEKLTSE-CIFREQFEENWYNTYSSNIYKHGNTGRR 164
QY 147 ----LPQKDSPNQDATSWGP---VRFLPMP 169
DB 165 YFVALNKDGTPRDGARSRRKQKFTHFLRP 194

RESULT 11
Q9HCT0 PRELIMINARY; PRT; 170 AA.
AC Q9HCT0;
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DE FGF-22.
GN FGF22.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Itoh N.;
RT "human FGF-22.";
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB012925; BAB13479.1; -.
SQ SEQUENCE 170 AA; 19662 MW; CB88918C2D54ACE7 CRC64;

Query Match 12.8%; Score 142.5; DB 4; Length 170;
Best Local Similarity 33.1%; Pred. No. 1.1e-05;
Matches 52; Conservative 24; Mismatches 66; Indels 15; Gaps 8;

QY 4 MRSRVGTGLG-LWVRLLAFLVLLGVYQAYPIPDSSPLQFGGQVQRORYLYTDDQDTEAHL 62
DB 1 MRRL-LWGLAWLLARAPDAAGTSPASRGRSYPHLE--GDVWRRLFS-----STHFFL 53
QY 63 EIREDTGVVGAHR-SPESLLELKALKPGVIOILGVKASRFLLCQPDGALYSGPHDFPEA 121
DB 54 RVDPGRGVQGTWRHGGQDSILRISRVGVVVIKAVSSGYVAMNRRGLYGRSLYTVD- 112
QY 122 CSFRELLEDGYNVYOSE---AHGLP--LRLPQKDSP 153
DB 113 CRFRERIEENGHTYASQRWRRRGQPMFLDRGGP 149

RESULT 12
O42407 PRELIMINARY; PRT; 212 AA.
AC O42407;
DT 01-JAN-1998 (Tremblrel. 05, Created)
DT 01-JUN-1998 (Tremblrel. 06, Last sequence update)
DE FTBROBLAST GROWTH FACTOR 10.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
OX NCBI_TaxID=9031;
```

```

[1]
SEQUENCE FROM N.A.
RP MEDLINE-97330690; PubMed-9187149;
RA Chuchi H., Nakagawa T., Yamamoto A., Araga A., Ohta T., Ishimaru Y.,
RA Yoshio H., Kuwana T., Nohno T., Yamasaki M., Itoh N., Noji S.;
RT "The mesenchymal factor, FGF10, initiates and maintains the outgrowth
RT of the chick limb bud through interaction with FGF8, an apical
RT ectodermal factor.";
RL Development 124:2235-2244(1997).
DR EMBL; D86333; BAA24945.1; -.
DR HSSP; P03968; 1BAR.
DR InterPro; IPR002209; -.
DR PFam; PF00167; FGF; 1.
DR PRINTS; PR00263; HBGFFGF.
DR ProDom; PD000831; -.
DR SMART; SM00442; FGF; 1.
SQ SEQUENCE 212 AA; 23631 MW; AB4C0B32C72A0D90 CRC64;

Query Match 12.7%; Score 141.5; DB 13; Length 212;
Best Local Similarity 31.1%; Pred. No. 1.8e-05;
Matches 38; Conservative 27; Mismatches 38; Indels 19; Gaps 5;

QY 29 AYPIDSSPL-----LQFGGQVQRORYLYTDDQDTEAHLEIREDTGVVGAHRS 77
DB 56 SFPSSPSSPSAGRHVNSYNHLQ--GDVRRKLYSYN----KYFLKIEKNGKVGSTKEN 109
QY 78 -PESLLELKALKPGVIOILGVKASRFLLCQPDGALYSGPHDFPEACSFRELLLEDGYNVY 136
DB 110 CPTSEILTSVEIGVAVKSIKSNYILAMNKGKVGSKFNSD-CKLKERIEENYNY 168
QY 137 QS 138
DB 169 AS 170

RESULT 13
Q9ESS2 PRELIMINARY; PRT; 162 AA.
AC Q9ESS2;
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE FGF-22.
GN FGF-22.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Itoh N.;
RT "mouse FGF-22.";
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB036765; BAB16407.1; -.
SQ SEQUENCE 162 AA; 18927 MW; 225EF512F4E1BE29 CRC64;

Query Match 12.5%; Score 139; DB 11; Length 162;
Best Local Similarity 30.9%; Pred. No. 2.2e-05;
Matches 55; Conservative 30; Mismatches 55; Indels 38; Gaps 11;

QY 4 MRSRVGTGLG-LWVRLLAFLVLLGVYQAYPIPDSSPLQFGGQVQRORYLYTDDQDTEAHL 62
DB 1 MRSRL-WLGLAW--LLLA-----RAPGAPGGYPHLE--GDVWRRLF-----SSTHF 42
QY 63 EIREDTGVVGAHR-SPESLLELKALKPGVIOILGVKASRFLLCQPDGALYSGPHDF 119
DB 43 FLRVDLGGVQGTWRHGGQDSIVRISRVGVVVIKAVISGYVAMNRRGLYGRSYV 102
QY 120 EACSFRELLEDGYNVYQS-----EAHGLPLRLPKQDSPNODATSWGPV 163
DB 103 D-CRFRERIEENGHTYASRWRHRRGPMFLALDSQGIPI-ROGRTRRHOLSTHFLPV 158
```

```

DR PRINTS; PR00262; ILIHBGF.
DR PROSITE; PS00247; HEGF_FGF; 1.
DR SMART; SM00442; FGF; 1.
SQ SEQUENCE 211 AA; 23498 MW; AB04608C16060CC1 CRC64;

Query Match                12.5%  Score 139;  DB 4;  Length 211;
Best Local Similarity      34.0%;  Pred. NO. 3.le-05;
Matches 51;  Conservative 15;  Mismatches 64;  Indels 20;  Gaps

Qy 33 PSSPILPFGGVQVRYLYTDDQDTAHLLEIREDTGVVGAARHSPSL---LELKALKP 89
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 52 PGAAQLAHLGLRLRRQLYCY-----RTGFHLQILPDGSVGT--RODHSLEGLFEISVAV 105

Qy 90 GVIQILGWASRFICQPDGALYGSHPHDEACSFRELLEDGYNVVQSE--ANGFLPLR- 148
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 106 GLVSGIRGVDSGILYLGMDNGELYGSEKLTSE-CIFREQPEENWYNTYSSNYIKHGDGTRR 164

Qy 147 ---LPQKDSNQDQATSNGP---VRFLPMP 169
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 165 YFVALNKDGTPRDGA SRKHQKFTHELPRP 194

Search completed: August 6, 2001, 21:09:09
Job time: 865 sec

```

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 6, 2001, 21:09:57 ; Search time 36.96 Seconds
(without alignments)
194.633 Million cell updates/sec

Title: US-09-391-861-4

Perfect score: 1115

Sequence: 1 MEMWRSRVGTGLWVRLLA.....SSDPLSMVPELQGRSPSYAS 210

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	262.5	23.5	216	1 FGFJ_HUMAN	O95750 homo sapien
2	207.5	18.6	218	1 FGFJ_MOUSE	O35622 mus musculus
3	178.5	16.0	208	1 FGF6_MOUSE	P21658 mus musculus
4	177.5	15.9	208	1 FGF6_HUMAN	P10767 homo sapien
5	171.5	15.4	206	1 FGF4_BOVIN	P48803 bos taurus
6	170.5	15.3	239	1 FGF3_HUMAN	P11487 homo sapien
7	170.0	15.2	187	1 FGF4_XENLA	P48805 xenopus lae
8	169.5	15.2	245	1 FGF3_MOUSE	P05524 mus musculus
9	166.5	14.9	194	1 FGF4_CHICK	P48804 gallus gall
10	165.5	14.8	206	1 FGF4_HUMAN	P08620 homo sapien
11	160.5	14.4	192	1 FGF4_XENLA	P48806 xenopus lae
12	158.5	14.2	256	1 FGF3_BRARE	P48802 brachydanio
13	155.5	13.9	202	1 FGF4_MOUSE	P11403 mus musculus
14	149.5	13.4	237	1 FGF3_XENLA	P36386 xenopus lae
15	149.0	13.4	264	1 FGF5_MOUSE	P15656 mus musculus
16	145.5	13.0	220	1 FGF3_CHICK	P48801 gallus gall
17	145.0	13.0	194	1 FGF7_SHEEP	P48808 ovis aries
18	145.0	13.0	266	1 FGF5_RAT	P48807 rattus norv
19	143.0	12.8	194	1 FGF7_HUMAN	P21781 homo sapien
20	142.5	12.8	155	1 FGF1_MESAU	P34004 mesocricetu
21	142.0	12.7	194	1 FGF7_MOUSE	P36363 mus musculus
22	142.0	12.7	208	1 FGF4_HUMAN	O15520 homo sapien
23	142.0	12.7	215	1 FGF4_RAT	P70492 rattus norv
24	141.5	12.7	155	1 FGF1_MOUSE	P10935 mus musculus
25	140.0	12.6	209	1 FGF4_MOUSE	O35655 mus musculus
26	140.0	12.6	268	1 FGF5_HUMAN	P12034 homo sapien
27	135.0	12.1	207	1 FGF6_HUMAN	O43320 homo sapien
28	134.0	12.0	154	1 FGF2_MOUSE	P15655 mus musculus
29	134.0	12.0	154	1 FGF2_RAT	P13109 rattus norv
30	133.5	12.0	155	1 FGF1_HUMAN	P05230 homo sapien
31	133.0	11.9	155	1 FGF2_BOVIN	P03969 bos taurus
32	133.0	11.9	155	1 FGF2_SHEEP	P20003 ovis aries
33	133.0	11.9	194	1 FGF7_RAT	Q02195 rattus norv

ALIGNMENTS

RESULT 1

ID	FGFJ_HUMAN	STANDARD;	PRT;	216 AA.
AC	O95750;			
DT	01-OCT-2000 (Rel. 40, Created)			
DT	01-OCT-2000 (Rel. 40, Last sequence update)			
DT	01-OCT-2000 (Rel. 40, Last annotation update)			
DE	FIBROBLAST GROWTH FACTOR-19 PRECURSOR (FGF-19).			
GN	FGF19.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Brain;			
EX	MEDLINE=99132028; PubMed=9931477;			
RA	Nishimura T., Utsunomiya Y., Hoshikawa M., Ohuchi H., Itoh N.;			
RT	"Structure and expression of a novel human FGF, FGF-19, expressed in the fetal brain."			
RT	the fetal brain."			
RL	Biochim. Biophys. Acta 1444:148-151(1999).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RA	Xie M.-H., Holcomb I., Deuel B., Dowd P., Huang A., Vagts A.,			
RA	Foster J., Brush J., Gu Q., Liang J., Hillan K., Goddard A.,			
RT	Gurney A.L.;			
RT	"FGF-19, a novel fibroblast growth factor with unique specificity for FGF4."			
RL	Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.			
CC	-!- FUNCTION: MAY BE INVOLVED IN BRAIN DEVELOPMENT DURING EMBRYOGENESIS.			
CC	-!- SUBCELLULAR LOCATION: SECRETED.			
CC	-!- TISSUE SPECIFICITY: EXPRESSED ONLY IN FETAL BRAIN.			
CC	-!- SIMILARITY: BELONGS TO THE HEPARIN-BINDING GROWTH FACTORS FAMILY.			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).			
CC	EMBL; AB018122; BAA75500.1; -			
DR	EMBL; AF110400; AAD45973.1; -			
DR	MIM; 603891; -			
DR	HSSP; P09038; 2BPH.			
DR	InterPro; IPR002209; -			
DR	InterPro; IPR002348; -			
DR	Pfam; PF00167; FGF; 1.			
DR	PRINTS; PR00262; ILIHBGF.			
DR	PRINTS; PR00263; HBGF_FGF.			
DR	PROSITE; PS00247; HBGF_FGF; 1.			
KW	Growth factor; Signal.			
FT	SIGNAL	1	22	POTENTIAL.
FT	CHAIN	23	216	FIBROBLAST GROWTH FACTOR-19.

34	132.5	11.9	155	1	FGF1_BOVIN	P03968 bos taurus
35	132	11.8	155	1	FGF2_HUMAN	P09038 homo sapien
36	131.5	11.8	208	1	FGF9_MOUSE	P31371 mus musculus
37	131.5	11.8	208	1	FGF9_MOUSE	P54130 mus musculus
38	131.5	11.8	208	1	FGF9_RAT	P36364 rattus norv
39	131	11.7	156	1	FGF2_MONDO	P48798 monodelphis
40	131	11.7	207	1	FGFG_RAT	O54769 rattus norv
41	131	11.7	209	1	FGF9_XENLA	Q91875 xenopus lae
42	129.5	11.6	152	1	FGF1_PIG	P20002 sus scrofa
43	128	11.5	155	1	FGF2_XENLA	P12226 xenopus lae
44	126	11.3	158	1	FGF2_CHICK	P48800 gallus gall
45	125	11.2	413	1	L756_CAEEL	Q11184 caenorhabdi

DR PRINTS; PR00263; HBGF.FGF.
 DR PROSITE; PS00247; HBGF_FGF; 1.
 KW Transforming protein; Oncogene; Growth factor; Mitogen; Signal;
 KW Glycoprotein.
 FT SIGNAL 1 ? POTENTIAL.
 FT CHAIN ? 208 FIBROBLAST GROWTH FACTOR-6.
 FT CARBOHYD 45 45 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT DISULFID 90 157 POTENTIAL.
 SQ SEQUENCE 208 AA; 22798 MW; BBE7B9301BB79A1B CRC64;

Query Match 16.0%; Score 178.5; DB 1; Length 208;
 Best Local Similarity 35.1%; Pred. No. 8.5e-09;
 Matches 47; Conservative 20; Mismatches 50; Indels 17; Gaps 5;

QY 43 GQVRQRYLYTDDQDTEAHLEIREDTGVVGAHRSPESLLELKALKPGVQIILGVKASRF 102
 DB 81 GIKRQRRLYC--NVGIGFHLQVPPDGRISGTHEENPYSLEISTVERGVVSLFGVKSALF 138
 QY 103 LCQPDGALYGSFHPDPEACSFRELLLEDGYNVYOSEAH-GLPLRLPQ-----KDSP 153
 DB 139 IANNSKGRLYTTPSFIDE-CKFREILLPNPNAYESDLYRGYIALSKYGRVKGSKVSP 197

QY 154 NQDATSWGPRVFLP 167
 DB 198 IMTVT-----HELP 206

RESULT 4
 FGF6_HUMAN STANDARD; PRT; 208 AA.
 ID FGF6_HUMAN
 AC P10767;
 DT 01-JUL-1989 (Rel. 11, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE FIBROBLAST GROWTH FACTOR-6 PRECURSOR (FGF-6) (HBGF-6) (HST-2).
 GN FGF6 OR HST2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-911360279; PubMed=1886714;
 RA Coullier F., Batoz M., Marics I., de Lapeyriere O., Birnbaum D.;
 RT "Putative structure of the FGF6 gene product and role of the signal
 peptide.";
 RL Oncogene 6:1437-1444 (1991).
 RN [2]
 RP SEQUENCE OF 11-208 FROM N.A.
 RX MEDLINE-92195660; PubMed=1549352;
 RA Iida S., Yoshida T., Naito K., Sakamoto H., Katoh O., Hirohashi S.,
 RA Sato T., Onda M., Sugimura T., Terada M.;
 RT "Human hst-2 (FGF-6) oncogene: cDNA cloning and characterization.";
 RL Oncogene 7:303-309 (1992).
 RN [3]
 RP SEQUENCE OF 81-208 FROM N.A.
 RX MEDLINE-89201880; PubMed=2649847;
 RA Marics I., Adelaide J., Raybaud F., Mattei M.-G., Coullier F.,
 RA Planche J., de Lapeyriere O., Birnbaum D.;
 RT "Characterization of the HST-related FGF.6 gene, a new member of the
 fibroblast growth factor gene family.";
 RL Oncogene 4:335-340 (1989).
 CC -1- FUNCTION: CAN TRANSFORM NIH 3T3 CELLS. EXHIBITS STRONG MITOGENIC
 AND ANGIOGENIC PROPERTIES.
 CC -1- SUBCELLULAR LOCATION: EXTRACELLULAR.
 CC -1- TISSUE SPECIFICITY: LEUKEMIA CELL LINES WITH PLATELET/
 MEGAKARYOCYTIC DIFFERENTIATION POTENTIAL.
 CC -1- SIMILARITY: BELONGS TO THE HEPARIN-BINDING GROWTH FACTORS FAMILY.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 the European Bioinformatics Institute. There are no restrictions on its

use by non-profit institutions as long as its content is in no way
 modified and this statement is not removed. Usage by and for commercial
 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 or send an email to license@isb-sib.ch).

CC EMBL; X57075; CAA40358.1;
 CC EMBL; X57075; CAA40359.1; ALT_INIT.
 CC EMBL; X57075; CAA40360.1; ALT_INIT.
 CC EMBL; X63454; CAA45054.1;
 CC EMBL; X14071; CAB37648.2;
 CC EMBL; X14072; CAB37648.2; JOINED.
 CC EMBL; X14073; CAB37648.2; JOINED.
 CC PIR; S04204; S04204.
 CC PIR; S23739; S23739.
 CC HSP; P09038; IBLD.
 CC MIN; I34921;
 CC InterPro; IPR002209;
 CC InterPro; IPR002348;
 CC Pfam; PF00167; FGF; 1.
 CC PRINTS; PR00262; IL1HBGF.
 CC PRINTS; PR00263; HBGF.FGF.
 CC PROSITE; PS00247; HBGF_FGF; 1.
 KW Transforming protein; Oncogene; Growth factor; Mitogen; Signal;
 KW Glycoprotein.
 FT SIGNAL 1 ? POTENTIAL.
 FT CHAIN ? 208 FIBROBLAST GROWTH FACTOR-6.
 FT CARBOHYD 45 45 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT DISULFID 90 157 POTENTIAL.
 FT CONFLICT 100 100 V->G (IN REF. 3).
 SQ SEQUENCE 208 AA; 22904 MW; 79EF44685B324322 CRC64;

Query Match 15.9%; Score 177.5; DB 1; Length 208;
 Best Local Similarity 34.3%; Pred. No. 1e-08;
 Matches 46; Conservative 21; Mismatches 50; Indels 17; Gaps 5;

QY 43 GQVRQRYLYTDDQDTEAHLEIREDTGVVGAHRSPESLLELKALKPGVQIILGVKASRF 102
 DB 81 GIKRQRRLYC--NVGIGFHLQVPPDGRISGTHEENPYSLEISTVERGVVSLFGVKSALF 138
 QY 103 LCQPDGALYGSFHPDPEACSFRELLLEDGYNVYOSEAH-GLPLRLPQ-----KDSP 153
 DB 139 VAMNSKGRLYATPSFQ-ECKFERETLLPNPNAYESDLYQGYIALSKYGRVKGSKVSP 197

QY 154 NQDATSWGPRVFLP 167
 DB 198 IMTVT-----HELP 206

RESULT 5
 FGF4_BOVIN STANDARD; PRT; 206 AA.
 ID FGF4_BOVIN
 AC P48803;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE FIBROBLAST GROWTH FACTOR-4 PRECURSOR (FGF-4) (HEPARIN SECRETORY
 DE TRANSFORMING PROTEIN) (HST) (HBGF-4).
 GN FGF4 OR HST.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Thymus;
 RX MEDLINE-96032369; PubMed=7557455;
 RA Yu J.C., Dessebra A.J., Wang L.M., Fleming T.P., Chedid M.,
 RA Miki T., Heideran M.A.;
 RT "An unexpected transforming gene in calf-thymus carrier DNA: bovine
 hst.";
 RL Gene 162:333-334 (1995).


```

DR HSP; P09038; 2BFH.
DR InterPro; IPR002209; -.
DR InterPro; IPR002348; -.
DR Pfam; PF00167; FGF; 1.
DR PRINTS; PR00262; IL1HBGF.
DR PRINTS; PR00263; HBGF.
DR PROSITE; PS00247; HBGF_FGF; 1.
KW Growth factor; Mitogen; Signal.
FT CHAIN 1 ? POTENTIAL.
FT SIGNAL 1 ? FIBROBLAST GROWTH FACTOR-4-I.
SQ SEQUENCE 187 AA; 21223 MW; AAE63D65E82AD1BD CRC64; 6;

Query Match 15.2%; Score 170; DB 1; Length 187;
Best Local Similarity 34.3%; Pred. No. 4.1e-08;
Matches 49; Conservative 22; Mismatches 52; Indels 20; Gaps 6;

QY 34 DSSPLQFGQVQRVLYTDDQDTEAHLEIREDTGVVGAHRSPELLELKALPGVIQ 93
DB 54 DSDYLL---GIRQRRLYC--NVGIGFHIQVLPDGRINGMHSNRYSLLELSPVEVGVS 108
QY 94 ILGVKASRLCQPDGALYSGHEDPEACSFRELLEDGYNVYQSEAH-GLPLRLPQ--- 149
DB 109 LYGVKSGMFVAMNAKGLYGRFEN-ECKFKETLLPNNYNAYESRKYPGMYIALGKNR 167
QY 150 -----KDSNQDATSGPVRFLP 167
DB 168 TTKGNRVSTWTLT-----HFLP 185

RESULT 8
FGF3_MOUSE STANDARD; PRT; 245 AA.
AC P05524;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE INT-2 PROTO-ONCOGENE PROTEIN PRECURSOR (FIBROBLAST GROWTH FACTOR-3)
DE (FGF-3) (HBGF-3).
GN FGF3 OR FGF-3 OR INT-2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86247582; PubMed=3013624;
RA Moore R., Casey G., Brookes S., Dixon M., Peters G., Dickson C.;
RT "Sequence, topography and protein coding potential of mouse int-2: a putative oncogene activated by mouse mammary tumour virus.";
RL EMBO J. 5:919-924(1986).
RN [2]
RP SEQUENCE OF 1-73 FROM N.A.
RX MEDLINE=88296404; PubMed=2841106;
RA Smith R., Peters G., Dickson C.;
RT "Multiple RNAs expressed from the int-2 gene in mouse embryonal carcinoma cell lines encode a protein with homology to fibroblast growth factors.";
RL EMBO J. 7:1013-1022(1988).
RN [3]
RP CHARACTERIZATION.
RX MEDLINE=91193291; PubMed=1964688;
RA Dickson C., Acland P., Smith R., Dixon M., Deed R., McAllan D., Walther W., Fuller-Pace F., Kiefer P., Peters G.;
RT "Characterization of int-2: a member of the fibroblast growth factor family.";
RL J. Cell Sci. Suppl. 13:87-96(1990).
CC -!- FUNCTION: COULD BE INVOLVED IN EAR DEVELOPMENT.
CC -!- INDUCTION: BY INTEGRATION OF MOUSE MAMMARY TUMOR VIRUS.
CC -!- SIMILARITY: BELONGS TO THE HEPARIN-BINDING GROWTH FACTORS FAMILY.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -

```

```

CC the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
CC -----
DR EMBL; Y00848; CAA68767.1; -.
DR PIR; A23930; TVMST2.
DR HSP; P09038; 2BFH.
DR MGD; MGI:95517; Fgf3.
DR InterPro; IPR002209; -.
DR InterPro; IPR002348; -.
DR Pfam; PF00167; FGF; 1.
DR PRINTS; PR00262; IL1HBGF.
DR PRINTS; PR00263; HBGF.
DR PROSITE; PS00247; HBGF_FGF; 1.
KW Transforming protein; Oncogene; Growth factor; Mitogen; Signal; Glycoprotein.
FT CHAIN 1 17 POTENTIAL.
FT SIGNAL 18 245 INT-2 PROTO-ONCOGENE PROTEIN.
FT CARBOHYD 65 65 N-LINKED (GLCNAC...).
SQ SEQUENCE 245 AA; 27214 MW; 70D94FD6A7837C79 CRC64;

Query Match 15.2%; Score 169.5; DB 1; Length 245;
Best Local Similarity 27.5%; Pred. No. 6.4e-08;
Matches 61; Conservative 21; Mismatches 63; Indels 77; Gaps 8;

QY 25 GYQAYIPDSSPLQFGQVQRVLYTDDQDTEAHLEIREDTGVVGAHRSPELLEL 84
DB 34 GWYE-----HLGGAPRRRLYC-----ATKYHLQLHPGSRVNGSLNSAYSILEI 78
QY 85 KALPKGVITQILGVKASRLCQPDGALYSGHEDPEACSFRELLEDGYNVYQSEAH--- 141
DB 79 TAVEGVVAINGLFSGRYLAAMKRGRLYADHYNAE-CEFVERIHELGINYASRLRTG 137
QY 142 -----GLPLRLPQKDSNQDATSGPVRFLP----- 167
DB 138 SSGPCAQRQPCAQRPWYVNVNGKGRPRGFKTRTKSS-----LFLPRLVGLHK 186
QY 168 ---MPGLLHEPDQA---GFLPPE-----PPDVGSSDPLS 196
DB 187 DHEVMVRLQSSQAPRAGSGQPRQRORRKKQSPQDHGRKMETLS 228

RESULT 9
FGF4_CHICK STANDARD; PRT; 194 AA.
AC P48804;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE FIBROBLAST GROWTH FACTOR-4 PRECURSOR (FGF-4) (HBGF-4).
GN FGF4 OR FGF-4.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95021713; PubMed=7935794;
RA Niswander L., Jeffrey S., Martin G.R., Tickle C.;
RT "A positive feedback loop coordinates growth and patterning in the vertebrate limb.";
RL Nature 371:609-612(1994).
CC -!- FUNCTION: MAY BE THE ENDOGENOUS RIDGE SIGNAL FOR LIMB DEVELOPMENT.
CC RECIPROCAL INTERACTIONS MAY CREATE A POSITIVE FEEDBACK LOOP BETWEEN SONIC HEDGEHOG (SHH) AND FGF4.
CC -!- TISSUE SPECIFICITY: POSTERIOR RIDGE.
CC -!- INDUCTION: BY RETINOIC ACID.
CC -!- SIMILARITY: BELONGS TO THE HEPARIN-BINDING GROWTH FACTORS FAMILY.
CC -----

```

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).

DR EMBL; U14654; AAA58706.1; -.
 DR HSP; P09038; 1BFF.
 DR InterPro; IPR002209; -.
 DR InterPro; IPR002348; -.
 DR Pfam; PF00167; FGF; 1.
 DR PRINTS; PR00262; ILIHGFG.
 DR PRINTS; PR00263; HBGFFGFG.
 DR PROSITE; PS00247; HBGF_FGF; 1.
 KW Growth factor; Mitogen; Signal.
 FT SIGNAL 1 ? POTENTIAL.
 FT CHAIN ? 194 FIBROBLAST GROWTH FACTOR-4.
 SQ SEQUENCE 194 AA; 21642 MW; 5D44245BE97E664A CRC64;

Query Match 14.9%; Score 166.5; DB 1; Length 194;
 Best Local Similarity 32.8%; Pred. No. 8.8e-08;
 Matches 44; Conservative 22; Mismatches 51; Indels 17; Gaps 5;

QY 43 GQVRYLYTDDQDQTEAHLETRDGTGVVGAHRSPELLELKALKPGVIOILGVKASRF 102

DB 67 GYKRLRLYC--NVGIFHIQVLPGRDIGHSENYRYSLEISPVGVSVFGRSLF 124

QY 103 LCOQPDGALYGSFHPDPEACSFRELLLEDGYNVQSEAH-GLPLRLPQ-----KDSP 153

DB 125 VAMNSKGLYSGTHVND-CKEKEILLPNVYSEKRYIPGVYIALSKNGRTKGNKVSP 183

QY 154 NQDATSWGVPVRLP 167

DB 184 TMTVT-----HFLP 192

RESULT 10

FGF4_HUMAN

ID FGF4_HUMAN STANDARD; PRT; 206 AA.

AC P08620;

DT 01-AUG-1988 (Rel. 08, Created)

DT 01-FEB-1996 (Rel. 33, Last sequence update)

DE FIBROBLAST GROWTH FACTOR-4 PRECURSOR (FGF-4) (HEPARIN SECRETORY

TRANSFORMING PROTEIN) (HST-1) (HST) (TRANSFORMING PROTEIN K53) (HBGF-

4).

GN FGF4 OR HST OR HSTF1 OR K53.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=88041096; PubMed=2959959;

RA Yoshida T., Miyagawa K., Odagiri H., Sakamoto H., Little P.F.R.,

RA Terada M., Sugimura T.;

RT Genomic sequence of hst, a transforming gene encoding a protein

homologous to fibroblast growth factors and the int-2-encoded

protein.";

RL Proc. Natl. Acad. Sci. U.S.A. 84:7305-7309(1987).

RN [2]

RP SEQUENCE FROM N.A.

RX MEDLINE=87204251; PubMed=2953031;

RA Taira M., Yoshida T., Miyagawa K., Sakamoto H., Terada M.,

RA Sugimura T.;

RT "cDNA sequence of human transforming gene hst and identification of

the coding sequence required for transforming activity.";

RL Proc. Natl. Acad. Sci. U.S.A. 84:2980-2984(1987).

RN [3]

RP SEQUENCE FROM N.A.

RX

RX MEDLINE=87301716; PubMed=2957062;
 RA Delli Bovi P., Curatola A.M., Kern F.G., Greco A., Ittmann M.,
 RA Basillio C.;

RT "An oncogene isolated by transfection of Kaposi's sarcoma DNA encodes

a growth factor that is a member of the FGF family.";

RL Cell 50:729-737(1987).

CC -1- FUNCTION: CAN TRANSFORM NIH 3T3 CELLS FROM A HUMAN STOMACH TUMOR

(HST) AND FROM KARPOSI'S SARCOMA (K53). IT HAS A MITOGENIC

ACTIVITY.

CC -1- SIMILARITY: BELONGS TO THE HEPARIN-BINDING GROWTH FACTORS FAMILY.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration

between the Swiss Institute of Bioinformatics and the EMBL outstation -

CC the European Bioinformatics Institute. There are no restrictions on its

CC use by non-profit institutions as long as its content is in no way

CC modified and this statement is not removed. Usage by and for commercial

CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).

CC EMBL; J02986; AAB59555.1; -.

DR EMBL; M17446; AAA59473.1; -.

DR PIR; A28417; TVHUHS.

DR HSP; P09038; 1BFF.

DR InterPro; IPR002209; -.

DR InterPro; IPR002348; -.

DR Pfam; PF00167; FGF; 1.

DR PRINTS; PR00262; ILIHGFG.

DR PRINTS; PR00263; HBGFFGFG.

DR PROSITE; PS00247; HBGF_FGF; 1.

KW Transforming protein; Oncogene; Growth factor; Mitogen; Signal.

FT SIGNAL 1 ? POTENTIAL.

FT CHAIN ? 206 FIBROBLAST GROWTH FACTOR-4.

SQ SEQUENCE 206 AA; 22047 MW; C7FD54A0272A1569 CRC64;

Query Match 14.8%; Score 165.5; DB 1; Length 206;

Best Local Similarity 36.2%; Pred. No. 1.2e-07;

Matches 42; Conservative 19; Mismatches 40; Indels 15; Gaps 4;

QY 61 HLETRDGTGVVGAHRSPELLELKALKPGVIOILGVKASRFLLCQPDGALYGSFHPDPE 120

DB 95 HLQALPDGRIGGAHADTRDLSLSPVGVSVFVASFVAMSKGLYSGFPTDE 154

QY 121 ACSFRELLLEDGYNVQSEAH-GLPLRLPQ-----KDSPQDATSWGVPVRLP 167

DB 155 -CFKEILLPNVYSEKRYIPGVYIALSKNGRTKGNRVSPMTKVT-----HFLP 204

RESULT 11

FGF4_XENLA

ID FGF4_XENLA STANDARD; PRT; 192 AA.

AC P48806;

DT 01-FEB-1996 (Rel. 33, Created)

DT 01-FEB-1996 (Rel. 33, Last sequence update)

DE FIBROBLAST GROWTH FACTOR-4-II PRECURSOR (FGF-4-II) (HBGF-4-II)

DE (EMBRYONIC FIBROBLAST GROWTH FACTOR II) (XERGF-II).

OS Xenopus laevis (African clawed frog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;

OC Xenopodinae; Xenopus.

OX NCBI_TaxID=8355;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=92315916; PubMed=1618138;

RA Isaacs H.V., Tannahill D., Slack J.M.W.;

RT "Expression of a novel FGF in the xenopus embryo. A new candidate

inducing factor for mesoderm formation and anteroposterior

specification.";

RL Development 114:711-720(1992).

CC -1- FUNCTION: GOOD CANDIDATE FOR AN INDUCING FACTOR WITH POSSIBLE

ROLES BOTH IN MESODERM INDUCTION AT THE BLASTULA STAGE AND IN THE


```
DR HSP; P09038; 2BFH.
DR MGD; MGI:95518; Fgf4.
DR InterPro; IPR002209; -.
DR PRINTS; PR002348; -.
DR Pfam; PF00167; FGF; 1.
DR PRINTS; PR00262; IL1HBGF.
DR PRINTS; PR00263; HBGF_FGF.
DR PROSITE; PS00247; HBGF_FGF; 1.
DR TRANSFORMING PROTEIN; Oncogene; Signal.
FT SIGNAL 1 202 FIBROBLAST GROWTH FACTOR-4.
FT CHAIN 167 167 A -> S (IN REF. 2).
FT CONFLICT 167 167
SQ SEQUENCE 202 AA; 62D456231047CA31 CRC64;

Query Match 13.9%; Score 155.5; DB 1; Length 202;
Best Local Similarity 33.6%; Pred. No. 8.5e-07;
Matches 39; Conservative 21; Mismatches 41; Indels 15; Gaps 4;

QY 61 HLEIREDTGVVGAHRSPELLEKALKPGVILGVKASRFLLCQPDGALYGSFHDPE 120
|::: || | : : ||||| : : || | : : | : | : | : | : | : | : |
Db 91 HLQVLPDGRIGGVHADTOSLLELSPVQGVVSIFGVASREFVAMSSRCKLFGVFFETDE 150
|::: || | : : ||||| : : || | : : | : | : | : | : | : | : |
QY 121 ACSFRELLEDGYNVQSEAH-GLPLRLPQ-----KDSNQDATSGPVRFLP 167
|::: || | : : ||||| : : || | : : | : | : | : | : | : | : |
Db 151 -CKEKEILLPNNYAYEAYPGFMALSKNGRTKKGKNGRVSTPMKVT-----HFLP 200

RESULT 14
FGF3_XENLA
ID FGF3_XENLA STANDARD; PRT; 237 AA.
AC P36386;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE FIBROBLAST GROWTH FACTOR-3 PRECURSOR (FGF-3) (HBGF-3) (INT-2).
GN FGF3.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RX MEDLINE=94038898; PubMed=8223431;
RA Kiefer P., Mathieu M., Close J.M., Peters G., Dickson C.;
RT "FGF3 from Xenopus laevis.";
RL EMBO J. 12:4159-4168(1993).
RN [2]
RP SEQUENCE OF 39-137 FROM N.A.
RC TISSUE=Neurula;
RX MEDLINE=93048831; PubMed=1425349;
RA Tannahill D., Isaacs H.V., Close M.J., Peters G., Slack J.M.W.;
RT "Developmental expression of the Xenopus int-2 (FGF-3) gene:
activation by mesodermal and neural induction.";
RL Development 115:695-702(1992).
CC -!- FUNCTION: POTENT MITOGEN AND TRANSFORMING AGENT.
CC -!- SIMILARITY: BELONGS TO THE HEPARIN-BINDING GROWTH FACTORS FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; Z25539; CAA80987.1; -.
CC EMBL; X65237; CAA46341.1; -.
CC PIR; S39582; S39582.
CC PIR; S25713; S25713.
CC HSP; P09038; 2BFH.
CC InterPro; IPR002209; -.

```

```
DR InterPro; IPR002348; -.
DR Pfam; PF00167; FGF; 1.
DR PRINTS; PR00262; IL1HBGF.
DR PRINTS; PR00263; HBGF_FGF.
DR PROSITE; PS00247; HBGF_FGF; 1.
DR GROWTH factor; Mitogen; Signal; Glycoprotein.
FT SIGNAL 1 237
FT CHAIN 22 237 FIBROBLAST GROWTH FACTOR-3.
FT CARBOHYD 83 83 N-LINKED (GLCNAC. ).
SQ SEQUENCE 237 AA; 26984 MW; EDD31B0893567A2D CRC64;

Query Match 13.4%; Score 149.5; DB 1; Length 237;
Best Local Similarity 33.9%; Pred. No. 3.4e-06;
Matches 40; Conservative 18; Mismatches 43; Indels 17; Gaps 4;

QY 25 GYQAYPIPDSPLLQFGQVQRVRYLYTDDQDTEAHLEIREDTGVVGAHR-SPELLE 83
|::: || | : : ||||| : : || | : : | : | : | : | : | : | : |
Db 52 GYVE-----HLGGAPNRKLYC-----ATKYHLQIHLNGKINGTLEKNSVFSLE 96
|::: || | : : ||||| : : || | : : | : | : | : | : | : | : |
QY 84 LKALKPGVILGVKASRFLLCQPDGALYGSFHDPEACSFRELLEDGYNVQSEAH 141
|::: || | : : ||||| : : || | : : | : | : | : | : | : | : |
Db 97 ITAVDVGIVAIKGLFSLAMNORGLYASETNPY-CEFEVRIHELGYNTYASRLY 153

RESULT 15
FGF5_MOUSE
ID FGF5_MOUSE STANDARD; PRT; 264 AA.
AC P15656;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE FIBROBLAST GROWTH FACTOR-5 PRECURSOR (FGF-5) (HBGF-5).
GN FGF5 OR FGF-5.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90201563; PubMed=2318343;
RA Hebert J.M., Basilio C., Goldfarb M., Haub O., Martin G.R.;
RT "Isolation of cDNAs encoding four mouse FGF family members and
characterization of their expression patterns during embryogenesis.";
RL Dev. Biol. 138:454-463(1990).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RX MEDLINE=91045929; PubMed=1700424;
RA Haub O., Drucker B., Goldfarb M.;
RT "Expression of the murine fibroblast growth factor 5 gene in the
adult central nervous system.";
RL Proc. Natl. Acad. Sci. U.S.A. 87:8022-8026(1990).
CC -!- SIMILARITY: BELONGS TO THE HEPARIN-BINDING GROWTH FACTORS FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; M30643; AAA96698.1; -.
CC EMBL; M37823; AAB02660.1; -.
CC EMBL; M37821; AAB02660.1; JOINED.
CC EMBL; M37822; AAB02660.1; JOINED.
CC EMBL; M37821; AAB02659.1; ALT_SEQ.
CC PIR; A36207; A36207.
CC PIR; B37360; B37360.
CC HSP; P09038; IBFC.
CC MGD; MGI:95519; Fgf5.
CC InterPro; IPR002209; -.

```

```
DR InterPro: IPR002348; -.
DR Pfam: PF00167; FGF; 1.
DR PRINTS; PR00262; ILIHGFG.
DR PRINTS; PR00263; HBGFEGF.
DR PROSITE; PS00247; HBGF_FGF; 1.
KW Transforming protein; Oncogene; Growth factor; Mitogen; Signal.
FT SIGNAL 1 17 POTENTIAL.
FT CHAIN 18 264 FIBROBLAST GROWTH FACTOR-5.
FT DOMAIN 53 59 POLY-SER.
FT CARBOHYD 108 108 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 264 AA; 29103 MW; F6A9C8153EE923D1 CRC64;

Query Match 13.4%; Score 149; DB 1; Length 264;
Best Local Similarity 25.0%; Pred. No. 4.3e-06;
Matches 52; Conservative 26; Mismatches 80; Indels 50; Gaps 6;

QY 35 SSPLQFGGQVRQRYLYTDDQDTEA-----HLEIREDTVVYGAHRSPESLLELK 85
Db 63 ASFGSGSGSEHSFOWSPSGRTGSLYCRVGIGFHLQIYPDGKVGNSHEASVLSILEIF 122
QY 86 ALKPGVIQILGVKASRFLCQCPDQALYGSFPHDFPEACSFRELLLEDGYNVYQSEAH--- 141
Db 123 AVSQGIVGIRGVFSNKFAMSKKGLHASAKFTDD-CKFRERFQENSNTYIYASAIHRTK 181
QY 142 -----GLPLRLPQKDSNQDATSWGVPVRFLLPMPGLLHEPQDQAGFL-- 182
Db 182 TGREWYVALMKRGKAKRGCSRV----KQHVSTHF-----LPRFKQSEQPELSFTVT 230
QY 183 -----PPEPPDYGSDPLSMVEFLQGR 204
Db 231 VPEKKPPVKPKVPLSQPRRSPSPVKYR 258
```

Search completed: August 6, 2001, 21:09:58
Job time: 724 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 6, 2001, 21:07:01 ; Search time 67.44 Seconds
(without alignments)
237.198 Million cell updates/sec

Title: US-09-391-861-4
Perfect score: 1115
Sequence: 1 MEWMRSRVGTGLWVRLLA.....SSDPLSMVEPLQGRSPSYAS 210

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_68: *
1: pir1: *
2: pir2: *
3: pir3: *
4: pir4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	235	21.1	251	JC7513	fibroblast growth
2	178.5	16.0	208	S14192	fibroblast growth
3	177.5	15.9	208	S20102	fibroblast growth
4	170.5	15.3	239	S04742	fibroblast growth
5	170	15.2	187	S23595	embryonic fibrobla
6	169.5	15.2	245	1 TWAST2	transforming prote
7	167.5	15.0	206	JC4268	fibroblast growth
8	166.5	14.9	194	2 I50710	fibroblast growth
9	165.5	14.8	206	1 TVHUHS	fibroblast growth
10	160.5	14.4	192	S54407	embryonic fibrobla
11	158.5	14.2	256	2 JC4627	fibroblast growth
12	155.5	13.9	202	1 TWMSHS	fibroblast growth
13	149.5	13.4	237	1 S39582	transforming prote
14	149	13.4	264	2 A36207	fibroblast growth
15	147	13.2	194	2 S26049	fibroblast growth
16	145.5	13.0	220	2 I50588	fibroblast growth
17	145	13.0	194	2 S49501	keratinocyte growt
18	145	13.0	266	2 S68144	fibroblast growth
19	143	12.8	194	1 A36301	fibroblast growth
20	142.5	12.8	155	1 A60721	acidic fibroblast
21	142	12.7	194	2 I48610	keratinocyte growt
22	141.5	12.7	155	2 S04147	acidic fibroblast
23	141.5	12.7	155	2 D37360	acidic fibroblast
24	139.5	12.5	267	1 TVHUFS	fibroblast growth
25	139	12.5	211	2 JC7353	fibroblast growth
26	138	12.4	212	3 JC7511	fibroblast growth
27	135	12.1	207	2 JC5941	fibroblast growth
28	134	12.0	154	2 A31674	basic fibroblast g
29	134	12.0	154	2 C37360	basic fibroblast g

30 133.5 12.0 155 1 A33665 acidic fibroblast
31 133 11.9 146 1 S00185 basic fibroblast g
32 133 11.9 157 1 GKBOB basic fibroblast g
33 132.5 11.9 155 1 GKBOB basic fibroblast g
34 132 11.8 210 2 A32398 basic fibroblast g
35 131.5 11.8 208 2 S66486 fibroblast growth
36 131.5 11.8 208 2 A48137 fibroblast growth
37 131 11.7 164 2 S31622 basic fibroblast g
38 131 11.7 207 2 JC5940 fibroblast growth
39 131 11.7 208 2 JC7082 fibroblast somatot
40 129.5 11.6 152 2 JH0476 acidic fibroblast
41 128 11.5 155 1 A40117 basic fibroblast g
42 126 11.3 189 2 A48834 basic fibroblast g
43 124.5 11.2 155 2 A60130 acidic fibroblast
44 123.5 11.1 137 2 I46711 fibroblast growth
45 123.5 11.1 155 2 JW0055 acidic fiblobrast

ALIGNMENTS

RESULT 1
JC7513
fibroblast growth factor-23 - mouse
C:Species: Mus musculus (house mouse)
C:Date: 31-Mar-2001 #sequence_revision 31-Mar-2001 #text_change 31-Mar-2001
C:Accession: JC7513
R:Iamashita, T.; Yoshioka, M.; Itoh, N.
Biochem. Biophys. Res. Commun. 277, 494-498, 2000
A:Title: Identification of a novel fibroblast growth factor, FGF-23, preferentially e
A:Reference number: JC7513; MUID:20490027
A:Contents: Embryo
A:Accession: JC7513
A:Molecule type: mRNA
A:Residues: 1-251 <YAM>
A:Cross-references: DDBJ:AB037889
C:Comment: This factor, a secreted protein, acts on proximal cells and plays roles in
C:Genetics:
A:Gene: fgf-23
C:Keywords: nucleus

Query Match 21.1%; Score 235; DB 3; Length 251;
Best Local Similarity 34.4%; Pred. No. 1.2e-13;
Matches 73; Conservative 30; Mismatches 81; Indels 28; Gaps 9;
QY 11 LGLWVRLLAFLVFL---LGVYQAYIPDSSPLL--QFGGQVRQRYLYTDDQDTEAHLEI 64
Db 2 LGTCLRLLVGLCTVCSIGTARAY--PDTSPLLGNNGLSLT---HLYTATAR-TSYHLQI 55
QY 65 REDGTVVGAHRSPESLELKALKPGVLIILGVKASRFLCQPDGALYSGSPHPDPEACSF 124
Db 56 HRDHVGTGTPHOTYTSALMITSEDAGSVITGATRRFLCMLHGNIFGSLHSPENCKF 115
QY 125 RELLEDGYNVYQSEAHGLPLRLPKDQSPNQDATSWGPV-RFLPMPG---LLH-----E 174
Db 116 RQWTELENGYDVLVSQKHLYLVSLGRKRIFQPGNPPFPFQFLARRNEVLLHFFYTVRPR 175
QY 175 PQDQAGFLPEPPVPGSDPLSMVEPLQGRSP 206
Db 176 RHTRSADPPPE-----RDPLNLVKPRPRATP 201

RESULT 2
S14192
fibroblast growth factor 6 - mouse
C:Species: Mus musculus (house mouse)
C:Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 17-Mar-2000
R:de Lapeyriere, O.; Rosnet, O.; Benharroch, D.; Raybaud, F.; Marchetto, S.; Planche,
Oncogene 5, 823-831, 1990
A:Title: Structure, chromosome mapping and expression of the murine Fgf-6 gene.
A:Reference number: S14192; MUID:90295275

Qy 61 HLEIREDTGVGAAHRSPESELLELKALKPGVIQLGVKASRFLCQQPDGALYGSHPFDPE 120
||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
Dd 95 HLQALPDGRIGGAHADTRDSLESLSVPERGVVISFGVASRRFFVAMSSKGKLYGSFPFTDE 154

Qy	84	LKALKPGV	IQILGV	KASRFL	CQPDG	ALYGS	PHFDE	ACSF	RELLED	GGYNYQ	SEAH	141	
		:	:	:	:	:	:	:	:	:	:	:	
Db	97	ITAVDVG	VVAIKG	LFSGRY	LAMNEK	GRLYA	SEVFN	RE	CEFL	RIHE	LGNTY	ASRHH	153

RESULT 12

TMMSHS
fibroblast growth factor 4 - mouse
N:Alternate names: transforming protein hstf1; transforming protein k-FGF; transforming
C:Species: Mus musculus (house mouse)
C:Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 17-Mar-2000
R:Accession: S04741; R37360
R:Brookes, S.; Smith, R.; Thurlow, J.; Dickson, C.; Peters, G.
Nucleic Acids Res. 17, 4037-4045, 1989
A:Title: The mouse homologue of hst/k-FGF: sequence, genome organization and location re
A:Reference number: S04741; MUID:89296455
A:Accession: S04741
A:Molecule type: DNA
A:Residues: 1-202 <BRO>
A:Cross-references: GB:X14849; GB:M28516; NID:g52791; PIDN:CAA32967.1; PID:g52792
R:Hebert, J.M.; Basilico, C.; Goldfarb, M.; Haub, O.; Martin, G.R.
Dev. Biol. 138, 454-463, 1990
A:Title: Isolation of cDNAs encoding four mouse FGF family members and characterization
A:Reference number: A37360; MUID:90201563
A:Accession: A37360
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-166, 'S', 168-202 <HEB>
A:Cross-references: GB:M30642; NID:g193290; PIDN:AAA37619.1; PID:g309237
C:Genetics:
A:Gene: hst
C:Superfamily: fibroblast growth factor
C:Keywords: growth factor; transforming protein

Query Match 13.9%; Score 155.5; DB 1; Length 202;
Best Local Similarity 33.6%; Pred. No. 1.1e-06;
Matches 39; Conservative 21; Mismatches 41; Indels 15; Gaps 4;
QY 61 HLEIRDTGVVGAHSPESLLEKALPGVIOILGVKASRLCQPDGALYGSHPDPE 120
DB 91 HLQVDPGRIGGVHADTRUSLLESPVQGVVSIFGVASRFVAMSSRGKFGVPFETDE 150
QY 121 ACSFRELLEDGYNVYQSAH-GLPLRLPQ-----KDSPLNQDATSGVPVRLFP 167
DB 151 -CKFKETLLPNVNYEAYVPGMFALSKNGRTKGNRVSTPMKVT-----HFLP 200

RESULT 13

transforming protein int-2 - African clawed frog
N:Alternate names: FGF-3 protein; fibroblast growth factor 3
C:Species: Xenopus laevis (African clawed frog)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
R:Kiefer, P.; Mathieu, M.; Close, M.J.; Peters, G.; Dickson, C.
EMBO J. 12, 4159-4168, 1993
A:Title: FGF3 from Xenopus laevis.
A:Reference number: S39582; MUID:94038898
A:Accession: S39582
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-237 <KIE>
A:Cross-references: EMBL:225539; NID:g396830; PIDN:CAA80987.1; PID:g396831
R:Tannahill, D.; Isaacs, H.V.; Close, M.J.; Peters, G.; Slack, J.M.W.
Development 115, 695-702, 1992
A:Title: Developmental expression of the Xenopus int-2 (FGF-3) gene: activation by mesod
A:Reference number: S25713; MUID:93048831
A:Accession: S25713
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 39-137 <TAN>
A:Cross-references: EMBL:X65237; NID:g64855; PIDN:CAA46341.1; PID:g64856
C:Superfamily: fibroblast growth factor

Query Match 13.4%; Score 149.5; DB 1; Length 237;
Best Local Similarity 33.9%; Pred. No. 4.7e-06;
Matches 40; Conservative 18; Mismatches 43; Indels 17; Gaps 4;

QY 25 GYQAYPIPDSSPLLQFGGQVRQRYLYTDDQDTEAHLEIRDTGVVGAHSPESLLE 83
DB 52 GYVE-----HLGAPNRKLYC-----ATYHLOIHLNGKINGTLEKNSVFSILE 96
QY 84 LKALPGVIOILGVKASRLCQPDGALYGSHPDPEACSFRELLEDGYNVYQSAH 141
DB 97 ITAVDVGIIVAIKGLFSGRYLA MNORGLRYASEYNPE-CEFERIHELGYNTYASRLY 153

RESULT 14

A36207
fibroblast growth factor 5 - mouse
C:Species: Mus musculus (house mouse)
C:Date: 28-Mar-1991 #sequence_revision 28-Mar-1991 #text_change 17-Mar-2000
R:Accession: A36207; B37360
R:Haub, O.; Drucker, B.; Goldfarb, M.
Proc. Natl. Acad. Sci. U.S.A. 87, 8022-8026, 1990
A:Title: Expression of the murine fibroblast growth factor 5 gene in the adult centra
A:Reference number: A36207; MUID:91045929
A:Accession: A36207
A>Status: preliminary; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-264 <HAU>
A:Cross-references: GB:M37821; GB:M37822; GB:M37823; NID:g193280; PIDN:AAB02660.1; PI
R:Hebert, J.M.; Basilico, C.; Goldfarb, M.; Haub, O.; Martin, G.R.
Dev. Biol. 138, 454-463, 1990
A:Title: Isolation of cDNAs encoding four mouse FGF family members and characterizati
A:Reference number: A37360; MUID:90201563
A:Accession: B37360
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-264 <HEB>
A:Cross-references: GB:M30643; NID:g193294; PIDN:AAA96698.1; PID:g309238
C:Superfamily: fibroblast growth factor

Query Match 13.4%; Score 149; DB 2; Length 264;
Best Local Similarity 25.0%; Pred. No. 6e-06;
Matches 52; Conservative 26; Mismatches 80; Indels 50; Gaps 6;

QY 35 SSPLLQFGGQVRQRYLYTDDQDTEA-----HLEIRDTGVVGAHSPESLLEK 85
DB 63 ASPGSGSGSEHSFQWSPSGRRTGSLYCRVIGIHLQIYDPDGKVGSHSASVLSILEIF 122
QY 86 ALKPGVIOILGVKASRLCQPDGALYGSHPDPEACSFRELLEDGYNVYQSAH---- 141
DB 123 AVSQGIVGIRGVFNSKFLAMSKGLHASAKFTDD-CKFEREQENSYNITYASAIHRTK 181
QY 142 -----GLPLRLPKDSPLNQDATSGVPVRLPMPGLLHPEPDQAGFL-- 182
DB 182 TGREWYVALNKRKAGKRGCSFRV---KQGVSTHF-----LPRFKSQEQELSFTVT 230
QY 183 -----PPEPPDVGSDPLSMVPLEQGR 204
DB 231 VPEKKKPPVPRKVPKPLSQPRRSPSPVKYR 258

RESULT 15

S26049
fibroblast growth factor 7 precursor - rat
N:Alternate names: keratinocyte growth factor
C:Species: Rattus norvegicus (Norway rat)
C:Date: 19-Mar-1998 #sequence_revision 19-Mar-1998 #text_change 16-Jul-1999
R:Accession: S26049; S78446
R:Van, G.; Nikolopoulos, S.; Wang, F.; McKeehan, W.L.
In Vitro Cell. Dev. Biol. 27, 437-438, 1991
A:Title: Sequence of rat keratinocyte growth factor (heparin-binding growth factor ty
A:Reference number: S26049
A:Accession: S26049

Query Match	13.28;	Score 147;	DB 2;	Length 194;
Best Local Similarity	28.98;	Pred. No. 6.le-06;		
Matches	41; Conservative	28; Mismatches	47; Indels	26; Gaps
QY	42	GGGQRVLYTDDDDTEAHLIEIEDGTGVVGAAH-RSPESLLEKALKPCVIQLGVKAS	100	
Db	61	GGDIRVRFLC-----RTQWYLRIDRKVKVGVTQMRSNYNMEIRIVAVGIYAIGVSE	116	
QY	101	RFLCOQPDPGALYGSPHPDEACSFRELLLEDGYNVYOS-----EAGHGLPR	146	
Db	117	VYLAMNKEGELYAKECN-EDCNFKELILEHNHYNTASYAKWTSHSGGEMFVALNQKGLPVK	175	
QY	147	LPOKOSPNO DATSGVPFRFLPM	168	
Db	176	--GKKTKKEQKTA----HFLEPM	191	

Search completed: August 6, 2001, 21:07:02
Job time: 1023 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 6, 2001, 21:05:42 ; Search time 18.95 Seconds
(without alignments)
228.178 Million cell updates/sec

Title: US-09-391-861-4
Perfect score: 1115
Sequence: 1 MEMRSRVGTGLWVRLLA.....SSDPLSMVEPLOGRSPSYAS 210

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 197339 seqs, 20590346 residues

Total number of hits satisfying chosen parameters: 197339

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2.6/prodata/1/iaa/5A_COMB.pep:*
2: /cgn2.6/prodata/1/iaa/5B_COMB.pep:*
3: /cgn2.6/prodata/1/iaa/6A_COMB.pep:*
4: /cgn2.6/prodata/1/iaa/6B_COMB.pep:*
5: /cgn2.6/prodata/1/iaa/PTCUS_COMB.pep:*
6: /cgn2.6/prodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	180	16.1	158	3	US-08-776-207-18
2	177.5	15.9	145	1	US-08-551-171-3
3	177.5	15.9	145	1	US-08-902-233-3
4	177.5	15.9	146	1	US-08-551-171-4
5	177.5	15.9	146	3	US-08-902-233-4
6	177.5	15.9	170	1	US-08-551-171-1
7	177.5	15.9	170	3	US-08-902-233-1
8	177.5	15.9	171	1	US-08-551-171-2
9	177.5	15.9	171	3	US-08-902-233-2
10	177.5	15.9	174	1	US-08-551-171-7
11	177.5	15.9	174	3	US-08-902-233-7
12	177.5	15.9	175	1	US-08-551-171-8
13	177.5	15.9	175	3	US-08-902-233-8
14	177.5	15.9	198	1	US-08-439-725A-14
15	177.5	15.9	198	1	US-08-441-629-12
16	177.5	15.9	198	2	US-08-867-471-14
17	177.5	15.9	198	2	US-08-438-439C-10
18	177.5	15.9	198	2	US-08-438-439C-20
19	177.5	15.9	198	3	US-08-718-904-15
20	177.5	15.9	198	3	US-09-023-082A-14
21	177.5	15.9	198	3	US-08-776-207-12
22	177.5	15.9	198	5	PCT-US95-09172-12
23	177.5	15.9	207	1	US-08-551-171-5
24	177.5	15.9	207	3	US-08-902-233-5
25	177.5	15.9	208	1	US-08-551-171-6
26	177.5	15.9	208	1	US-08-462-169B-16
27	177.5	15.9	208	1	US-08-462-169B-14

28	177.5	15.9	208	2	US-08-207-412B-11	Sequence 11, Appl
29	177.5	15.9	208	2	US-08-951-822-27	Sequence 27, Appl
30	177.5	15.9	208	3	US-09-103-079-14	Sequence 14, Appl
31	177.5	15.9	208	3	US-08-902-233-6	Sequence 6, Appl
32	177.5	15.9	208	3	US-09-093-585-16	Sequence 16, Appl
33	170.5	15.3	239	1	US-08-464-590A-11	Sequence 11, Appl
34	170.5	15.3	239	1	US-08-462-169B-11	Sequence 11, Appl
35	170.5	15.3	239	2	US-08-207-412B-14	Sequence 14, Appl
36	170.5	15.3	239	2	US-08-951-822-35	Sequence 35, Appl
37	170.5	15.3	239	3	US-03-103-079-11	Sequence 11, Appl
38	170.5	15.3	239	3	US-08-718-904-12	Sequence 12, Appl
39	170.5	15.3	239	3	US-09-023-082A-21	Sequence 21, Appl
40	170.5	15.3	239	3	US-09-093-585-11	Sequence 11, Appl
41	170	15.2	187	1	US-08-441-629-11	Sequence 11, Appl
42	170	15.2	187	3	US-08-776-207-11	Sequence 11, Appl
43	170	15.2	187	5	PCT-US95-09172-11	Sequence 11, Appl
44	169.5	15.2	245	1	US-08-439-725A-11	Sequence 11, Appl
45	169.5	15.2	245	2	US-08-867-471-11	Sequence 11, Appl

ALIGNMENTS

RESULT 1
US-08-776-207-18
; Sequence 18, Application US/08776207A
; Patent No. 6080718
; GENERAL INFORMATION:
; APPLICANT: Kirschner, Marc W.
; APPLICANT: Kinoshita, No. 6080718iyuki
; TITLE OF INVENTION: Receptor-Ligand Assay
; FILE REFERENCE: HU95-01A2
; CURRENT APPLICATION NUMBER: US/08/776.207A
; CURRENT FILING DATE: 1997-06-23
; EARLIER APPLICATION NUMBER: PCT/US95/09172
; EARLIER FILING DATE: 1995-07-19
; EARLIER APPLICATION NUMBER: 08/441.629
; EARLIER FILING DATE: 1995-05-15
; EARLIER APPLICATION NUMBER: 08/279.217
; EARLIER FILING DATE: 1994-07-22
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 18
; LENGTH: 158
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: artificial
US-08-776-207-18

Query Match 16.1%; Score 180; DB 3; Length 158;
Best Local Similarity 39.3%; Pred. No. 1.le-11;
Matches 53; Conservative 12; Mismatches 50; Indels 20; Gaps 5;
QY 43 GQVRVLYTDDQDTEAHLEIREDTGVGAHRSPELLEKALPGVIOILGVKASRF 102
I: | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
Db 33 GKRTFRLLYC---RVGGFHLQLPDGRVNGTHESNRYSLLELSAVEGVSVIKGVESCLF 89
QY 103 LCQQPDGALYSGPHDPDPCSFRELLEDDGYNVYQS-----FAHGLPLRLPKQDS 152
I: | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
Db 90 LAMNKKGLYASKKP-TTECKFKERLLENTYASAKRYGMYVALNKNRPRK-RGSKTS 147
QY 153 PNQDATSGNPVRFLP 167
Db 148 PTKKAT-----HFLP 157

RESULT 2
US-08-551-171-3
; Sequence 3, Application US/08551171
; Patent No. 5679550
; GENERAL INFORMATION:

```
; APPLICANT: YOSHIMURA, Koji
; APPLICANT: ISHIMARU, Kaori
; APPLICANT: IGARASHI, Koichi
; APPLICANT: TERADA, Masaaki
; TITLE OF INVENTION: hst-2 MUTEIN, DNA CODING FOR THE SAME AND
; TITLE OF INVENTION: PREPARATION THEREOF
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &
; CUSHMAN
; STREET: 130 Water Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: US
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/551.171
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/196.001
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: NEUNER, George W
; REGISTRATION NUMBER: 26964
; REFERENCE/DOCKET NUMBER: 44146
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)523-3400
; TELEFAX: (617)523-6440
; TELEX: 200291 STRE UR
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 145 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-551-171-3

Query Match 15.9%; Score 177.5; DB 1; Length 145;
Best Local Similarity 34.3%; Pred. No. 1.8e-11;
Matches 46; Conservative 21; Mismatches 50; Indels 17; Gaps 5;

QY 43 GQVQRRLYTDDQDTEAHLEIREDTGVVGAHRSPESLLELKALPGVIOILGVKASRF 102
| ||| || : ||: || : || || || : || || || : || || || : || || ||
Db 18 GIKRQRRLYC--NVGIGFHLQVLPDGRISGTHEENPYSLLLEISTVERGVSLFGVRSALF 75

QY 103 LCQQPDGALYGSFHPDPEACSFRELLLEDGYNVYQSEAH-GLPLRLPQ-----KDSP 153
: ||| || | || || || || || || || || || || || || || || || || ||
Db 76 VAMNSKGRLYATPSFQ-ECKFRETLLPNNINAYESDLYOGTYIALSKYGRVKRGSKVSP 134

QY 154 NQDATSWGPFVRFLP 167
| |||
Db 135 IMTVT-----HFLP 143

RESULT 3
US-08-233-3
; Sequence 3, Application US/08502233
; Patent No. 6013784
; GENERAL INFORMATION:
; APPLICANT: YOSHIMURA, Koji
; APPLICANT: ISHIMARU, Kaori
; APPLICANT: IGARASHI, Koichi
; APPLICANT: TERADA, Masaaki
; TITLE OF INVENTION: hst-2 MUTEIN, DNA CODING FOR THE SAME AND
; TITLE OF INVENTION: PREPARATION THEREOF
; NUMBER OF SEQUENCES: 10
```

```
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &
; CUSHMAN
; STREET: 130 Water Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: US
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/902.233
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/196.001
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: NEUNER, George W
; REGISTRATION NUMBER: 26964
; REFERENCE/DOCKET NUMBER: 44146
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)523-3400
; TELEFAX: (617)523-6440
; TELEX: 200291 STRE UR
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 145 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-902-233-3

Query Match 15.9%; Score 177.5; DB 3; Length 145;
Best Local Similarity 34.3%; Pred. No. 1.8e-11;
Matches 46; Conservative 21; Mismatches 50; Indels 17; Gaps 5;

QY 43 GQVQRRLYTDDQDTEAHLEIREDTGVVGAHRSPESLLELKALPGVIOILGVKASRF 102
| ||| || : ||: || : || || || : || || || : || || || : || || ||
Db 18 GIKRQRRLYC--NVGIGFHLQVLPDGRISGTHEENPYSLLLEISTVERGVSLFGVRSALF 75

QY 103 LCQQPDGALYGSFHPDPEACSFRELLLEDGYNVYQSEAH-GLPLRLPQ-----KDSP 153
: ||| || | || || || || || || || || || || || || || || || || ||
Db 76 VAMNSKGRLYATPSFQ-ECKFRETLLPNNINAYESDLYOGTYIALSKYGRVKRGSKVSP 134

QY 154 NQDATSWGPFVRFLP 167
| |||
Db 135 IMTVT-----HFLP 143

RESULT 4
US-08-551-171-4
; Sequence 4, Application US/08551171
; Patent No. 5679550
; GENERAL INFORMATION:
; APPLICANT: YOSHIMURA, Koji
; APPLICANT: ISHIMARU, Kaori
; APPLICANT: IGARASHI, Koichi
; APPLICANT: TERADA, Masaaki
; TITLE OF INVENTION: hst-2 MUTEIN, DNA CODING FOR THE SAME AND
; TITLE OF INVENTION: PREPARATION THEREOF
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &
; CUSHMAN
; STREET: 130 Water Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: US
```


Query Match 15.9%; Score 177.5; DB 3; Length 146;
Best Local Similarity 34.3%; Pred. No. 1.8e-11;
Matches 46: Conservative 21; Mismatches 50; Indels 17

0v 43 GOVRORYLYTDDDDODTEAHLEIREDDGTVVGAARRSPESLLELKALKPGVIOILGVKASRF 102

DB 19 GIKRQRRLYC--NVGIGFFHLQVLPDGRISGTHEENPYSLLEISITVERGVVSLFVGVRSALE 76

QY IO3 LCQQFDGALIGSFHFDPACSFRELLLEDGINVIQSEAH-GLFLRLFQ-----KDSF IO3

DD // VAMNSAGRLIATPSFQ-EECAFREITLLPNNINAIYESDLIQTIIALSNIGRVAKRGSNVSF 133

QY TS# NQJ813M9EAFKEEF TO7

|||

|

22 OCT 1971

RESULT 6

; Sequence 1, Application US

; GENERAL INFORMATION:

APPLI
APPLI

US-08-902-233-4

TITLE

;
TITLE OF INVENT

; NUMBER OF SEQUENCES: 10

; CORRESPONDENCE ADDRESS:
: ADDRESSEE: DAVID C. CONT.

ADDRESSEE: DAVID G. CONL
ADDRESSEE: CUSHMAN

ADDRESSEE: CUSHMAN
STREET: 130 Water Street

CITY: Boston

STATE: Massachusetts

; COUNTRY: US

```

; ZIP: 02109

```

```

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

```

```

;
; MEDIUM TYPE: Floppy disk
;
; COMPUTER: IBM PC compatible

```

```

;
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS

```

; OPERATING SYSTEM: FC DOS;
; SOFTWARE: PatentIn Release

```

;
;
; CURRENT APPLICATION DATA:

```

APPLICATION NUMBER: US/01

;
FILING DATE:

; CLASSIFICATION: 530

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER. USC /O

; APPLICATION NUMBER: US/0
 ; FILING DATE:

FILED DATE: 11/15/2011
ATTORNEY/AGENT INFORMATION:

ATTORNEY/AGENT INFORMATION:

```

; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 170 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-902-233-1

Query Match          15.9%; Score 177.5; DB 3; Length 170;
Best Local Similarity 34.3%; Pred No. 2.3e-11;
Matches 46; Conservative 21; Mismatches 50; Indels 17; Gaps

QY 43 GOVQRQRYLYTDDQDTEAHLREITDGTGVGAHRSPESLLELKALKPQGVQILGVKASRF 102
      | ||| || : ||: || : | : |||| : ||: ||: ||: ||: ||: |
Db 43 GIKRQRRLYC--NVGIGFHLQVLPGDRISGTHEENPYSLLEISTVERGVVSLFGVRSALF 100

QY 103 LCOOPGALYGSHPHDEACSFRELLEDCGVNYQSEAH-GLPLRLPQ-----KDSP 153
      : ||| : | | ||| || | ||| : | : | : | : | : | : |
Db 101 VAMNSKGRLYATPSFQ-EECKFRETLPPNNYAYESDLYQGTVIALSKYGRVKRGSKVSP 159

QY 154 NQDATSGWGPVREL P 167
      | |||
Db 160 IMTVT-----HFLP 168

RESULT 8
US-08-551-171-2
; Sequence 2, Application US/08551171
; Patent No. 5679550
; GENERAL INFORMATION:
; APPLICANT: YOSHIMURA, Koji
; APPLICANT: ISHIMARU, Kaori
; APPLICANT: IGARASHI, Koichi
; APPLICANT: TERADA, Masaki
; TITLE OF INVENTION: hst-2 MUTEIN, DNA CODING FOR THE SAME AND
; TITLE OF INVENTION: PREPARATION THEREOF
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &
; ADDRESSEE: CUSHMAN
; STREET: 130 Water Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: US
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/551,171
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/196,001
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: NEUNER, George W
; REGISTRATION NUMBER: 26964
; REFERENCE/DOCKET NUMBER: 44146
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)523-3400
; TELEFAX: (617)523-6440
; TELEX: 200291 STRE UR
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 171 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-551-171-2

```

Query Match	15.9%;	Score	177.5;	DB 1;	Length	171;
Best Local Similarity	34.3%;	Pred. No.	2.3e-11;			
Matches	46;	Conservative	21;	Mismatches	50;	Indels 17; Gaps
QY	43	GQVRYQLYTDQDTEAHLEIREDCVTVCAAHRSLSLELKALPGVQIILGVKASRF	102			
Db	44	GIRKQRLYC--NVGTFHLQVLDPGRIGSTHEENPYLSLEITVERGVVSFLFGVRSALF	101			
QY	103	LCQOQPDGALGSPHFDPEACSFRELLEGGYNNVQSEAH-GIPLRLPQ-----KDSP	153			
Db	102	VAMNSKGRUYATPSFQ-EECKFRETLLPNNYAYESDLYQGYIYALSIGRYVRKGSVSP	160			
QY	154	NQDATSWGPRVFLP	167			
Db	161	IMTVT-----HFLP	169			

```

RESULT 9
US-08-902-233-2
; Sequence 2, Application US/08902233
; Patent No. 6013784
; GENERAL INFORMATION:
; APPLICANT: YOSHIMURA, Koji
; APPLICANT: ISHIMARU, Kaori
; APPLICANT: IGARASHI, Koichi
; APPLICANT: TERADA, Masaaki
; TITLE OF INVENTION: hst-2 MUTEIN, DNA CODING FOR THE SAME AND
; TITLE OF INVENTION: PREPARATION THEREOF
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERT'S &
; ADDRESS: CUSHMAN
; STREET: 130 Water Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: US
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/902,233
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/196,001
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: NEUNER, George W
; REGISTRATION NUMBER: 26964
; REFERENCE/DOCKET NUMBER: 44146
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)523-3400
; TELEFAX: (617)523-6440
; TELEX: 200291 STRE UR
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 171 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-902-233-2

```

Query Match 15.9%; Score 177.5; DB 3; Length 171;
Best Local Similarity 34.3%; Pred. No. 2.3e-11;
Matches 46; Conservative 21; Mismatches 50; Indels 17; Gaps 5;
QY 43 GQVQRQLYTDQDQTEAHLFIREDGTGVGAHRSPSLLEKALRPGVTQLGKVASRF 102

```

Db      44 GIKQRRLYC--NVGICFHLOVLDGRISGTHRENPYSLLLEISTVERGVVSLFGVRSALF 101
QY     103 LCOOPDGAALYGSPHFDPEACSFRELLLEDGYYNYQVSAH-GLPLRLPQ-----KDSP 153
Db      102 VAMNSKGRLYATTSFQ-EECKFRFETLLPNNNYAYESDLYOQTIALSKYGRVKRGSKVSP 160
QY     154 NQDATSWGPNVRELP 167
Db      161 IMTWT-----HFLP 169

RESULT 10
US-08-551-171-7
; Sequence 7, Application US/08551171
; Patent No. 5679550
; GENERAL INFORMATION:
; APPLICANT: YOSHIMURA, Koji
; APPLICANT: ISHIMARU, Kaori
; APPLICANT: IGARASHI, Koichi
; APPLICANT: TERADA, Masaaki
; TITLE OF INVENTION: hst-2 MUTEIN, DNA CODING FOR THE SAME AND
; TITLE OF INVENTION: PARTITION THEREOF
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &
; ADDRESSEE: CUSHMAN
; STREET: 130 Water Street
; City: Boston
; STATE: Massachusetts
; COUNTRY: US
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/551,171
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/196,001
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: NEUNER, George W
; REGISTRATION NUMBER: 26964
; REFERENCE/DOCKET NUMBER: 44146
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)523-3400
; TELEFAX: (617)523-6440
; TELEX: 200291 STRE UR
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 174 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-551-171-7

```

		Query Match	15.9%	Score 177.5;	DB 1; Length 174;
		Best Local Similarity	34.3%;	Pred. No. 2.3e-11;	
		Matches	46;	Conservative	21; Mismatches 50; Indels 17; Gaps 5;
Qy	43	GQVRQLYLTDDQDTEAHLREIDGTVVGAAHRSPELSLELKALKPGVIOLGVGASRF	102		
Dd	47	GIKRQRRLYC--NVGIGFHLQVLDPGRISGTHEENPYSLLETSTVERGVSVLFGVSALF	104		
Qy	103	LCCQPDGALYGSPHPDPBACSFRELLEDGYNVOYEAH-GUPLKLPO-----KDSP	153		
Dd	105	VAMNSKGRIATPSPFO-BECKPFRTLLPNNNAYVESDLIOGYNTIALSKYGRVKRGSKYSVP	163		

QY 154 NQDATSWGVPVRLP 167
Db 164 INTVT-----HFLP 172

RESULT 11
US-08-902-233-7
; Sequence 7, Application US/08902233
; Patent No. 6013784
; GENERAL INFORMATION:
; APPLICANT: YOSHIMURA, Koji
; APPLICANT: ISHIMARU, Kaori
; APPLICANT: IGARASHI, Koichi
; APPLICANT: TERADA, Masaaki
; TITLE OF INVENTION: hst-2 MUTEIN, DNA CODING FOR THE SAME AND
; TITLE OF INVENTION: PREPARATION THEREOF
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &
; ADDRESSEE: CUSHMAN
; STREET: 130 Water Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: US
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/902.233
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/196.001
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: NEUNER, George W
; REGISTRATION NUMBER: 26964
; REFERENCE/DOCKET NUMBER: 44146
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)523-3400
; TELEFAX: (617)523-6440
; TELEX: 200291 STRE UR
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 174 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-902-233-7

Query Match 15.9%; Score 177.5; DB 3; Length 174;
Best Local Similarity 34.3%; Pred. No. 2.3e-11;
Matches 46; Conservative 21; Mismatches 50; Indels 17; Gaps 5;
QY 43 GQVRRLYTDQDTEAHLREDTGVVGAHRSPELLELKALKPGVQILGVKASRF 102
Db 47 GIKRRLRYC--NVGIGFHLQVLPDGRISGTHEENPYSLEISTVERGVSLFGVRSALF 104
QY 103 LCOOPDGALYSPHFDPAACSFRELLLEDGYNVYQSEAH-GILPLRLPQ-----KDSP 153
Db 105 VAMNSKGLRYATPSFQ-ECKFRETLLPNYNNAYESDLYQGTIYALSKEYGRVKGSKVSP 163
QY 154 NQDATSWGVPVRLP 167
Db 164 INTVT-----HFLP 172

RESULT 12
US-08-551-171-8

; Sequence 8, Application US/08551171
; Patent No. 5679550
; GENERAL INFORMATION:
; APPLICANT: YOSHIMURA, Koji
; APPLICANT: ISHIMARU, Kaori
; APPLICANT: IGARASHI, Koichi
; APPLICANT: TERADA, Masaaki
; TITLE OF INVENTION: hst-2 MUTEIN, DNA CODING FOR THE SAME AND
; TITLE OF INVENTION: PREPARATION THEREOF
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &
; ADDRESSEE: CUSHMAN
; STREET: 130 Water Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: US
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/551.171
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/196.001
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: NEUNER, George W
; REGISTRATION NUMBER: 26964
; REFERENCE/DOCKET NUMBER: 44146
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)523-3400
; TELEFAX: (617)523-6440
; TELEX: 200291 STRE UR
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 175 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-551-171-8
Query Match 15.9%; Score 177.5; DB 1; Length 175;
Best Local Similarity 34.3%; Pred. No. 2.4e-11;
Matches 46; Conservative 21; Mismatches 50; Indels 17; Gaps 5;
QY 43 GQVRRLYTDQDTEAHLREDTGVVGAHRSPELLELKALKPGVQILGVKASRF 102
Db 48 GIKRRLRYC--NVGIGFHLQVLPDGRISGTHEENPYSLEISTVERGVSLFGVRSALF 105
QY 103 LCOOPDGALYSPHFDPAACSFRELLLEDGYNVYQSEAH-GILPLRLPQ-----KDSP 153
Db 106 VAMNSKGLRYATPSFQ-ECKFRETLLPNYNNAYESDLYQGTIYALSKEYGRVKGSKVSP 164
QY 154 NQDATSWGVPVRLP 167
Db 165 INTVT-----HFLP 173
RESULT 13
US-08-902-233-8
; Sequence 8, Application US/08902233
; Patent No. 6013784
; GENERAL INFORMATION:
; APPLICANT: YOSHIMURA, Koji
; APPLICANT: ISHIMARU, Kaori
; APPLICANT: IGARASHI, Koichi
; APPLICANT: TERADA, Masaaki

STATE: CA

APPLCATION NUMBER: US 08/279,217
FILING DATE: 22-JUL-1994

```

; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32,227
; REFERENCE/DOCKET NUMBER: H095-01A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 861-6240
; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 198 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-441-629-12

```

```

Query Match      15.9%; Score 177.5; DB 1; Length 198;
Best Local Similarity 34.3%; Pred. No. 2.8e-11;
Matches 46; Conservative 21; Mismatches 50; Indels 17; Gaps 5;

QY  43  GQVRQRLYTDDQDTEAHLEIREDTGVVGAHRSPELLELKALKPGVIOILGVKASRF 102
      | ||| || : ||: || : || || || || || || || || || || || || ||
Db   71  GIKRQRRLYC--NVGIGFHLQVLPDGRISGTHEENPYSLLEISTVERGVWSLFGVRSALF 128

QY  103  LCQPPDGALYGSFHPDPEACSPRELLLEDGYNVYOSEAH-GLPLRLPO-----KDSP 153
      : ||| :|| | | || || || || || || || || || || || || || || ||
Db   129  VAMNSKGRLYATPSFQ-EECKFRETLPPNNYAYESDLYQGYTIALSKYGRVKRGSKVSP 187

QY  154  NODATSWGPPVRELP 167
      | |||
Db   188  IMTVT-----HFLP 196

```

Search completed: August 6, 2001, 21:05:43
Job time: 1064 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 6, 2001, 20:57:48 ; Search time 64.04 Seconds
(without alignments)
198.798 Million cell updates/sec

Title: US-09-391-861-4

Perfect score: 1115

Sequence: 1 MEMMSRVGTGLWVRLLA.....SSDPLSMVEPQGRSPSYAS 210

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 412676 seqs, 60623988 residues

Total number of hits satisfying chosen parameters: 412676

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A_Geneseq_0601.*
1: /SID88/gcgdata/geneseq/geneseq/AA1980.DAT.*
2: /SID88/gcgdata/geneseq/geneseq/AA1981.DAT.*
3: /SID88/gcgdata/geneseq/geneseq/AA1982.DAT.*
4: /SID88/gcgdata/geneseq/geneseq/AA1983.DAT.*
5: /SID88/gcgdata/geneseq/geneseq/AA1984.DAT.*
6: /SID88/gcgdata/geneseq/geneseq/AA1985.DAT.*
7: /SID88/gcgdata/geneseq/geneseq/AA1986.DAT.*
8: /SID88/gcgdata/geneseq/geneseq/AA1987.DAT.*
9: /SID88/gcgdata/geneseq/geneseq/AA1988.DAT.*
10: /SID88/gcgdata/geneseq/geneseq/AA1989.DAT.*
11: /SID88/gcgdata/geneseq/geneseq/AA1990.DAT.*
12: /SID88/gcgdata/geneseq/geneseq/AA1991.DAT.*
13: /SID88/gcgdata/geneseq/geneseq/AA1992.DAT.*
14: /SID88/gcgdata/geneseq/geneseq/AA1993.DAT.*
15: /SID88/gcgdata/geneseq/geneseq/AA1994.DAT.*
16: /SID88/gcgdata/geneseq/geneseq/AA1995.DAT.*
17: /SID88/gcgdata/geneseq/geneseq/AA1996.DAT.*
18: /SID88/gcgdata/geneseq/geneseq/AA1997.DAT.*
19: /SID88/gcgdata/geneseq/geneseq/AA1998.DAT.*
20: /SID88/gcgdata/geneseq/geneseq/AA1999.DAT.*
21: /SID88/gcgdata/geneseq/geneseq/AA2000.DAT.*
22: /SID88/gcgdata/geneseq/geneseq/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1115	100.0	210	21	AAB18636
2	603.5	54.1	153	22	AAB73069
3	262.5	23.5	216	20	Human fibroblast g
4	262.5	23.5	216	20	Human PRO533 prote
5	262.5	23.5	216	20	Amino acid sequenc
6	262.5	23.5	216	20	FGF-8 homologue PR
7	262.5	23.5	216	21	Human PRO533 prote
8	262.5	23.5	216	21	Human PRO533 amino
9	262.5	23.5	216	22	Human PRO533
10	262.5	23.5	216	22	Amino acid sequenc
11	257	23.0	215	20	Human PRO533 prote

12	256.5	23.0	214	20	AA08581
13	241	21.6	251	22	AA085297
14	207.5	18.6	142	22	AA073070
15	207.5	18.6	213	20	AA08582
16	183	16.4	175	15	AA08556
17	177.5	15.9	146	15	AA08554
18	177.5	15.9	171	15	AA08553
19	177.5	15.9	198	16	AA080781
20	177.5	15.9	198	16	AA080781
21	177.5	15.9	198	16	AA080781
22	177.5	15.9	198	16	AA080781
23	177.5	15.9	198	16	AA080781
24	177.5	15.9	198	16	AA080781
25	177.5	15.9	198	16	AA080781
26	177.5	15.9	198	16	AA080781
27	177.5	15.9	198	16	AA080781
28	177.5	15.9	198	16	AA080781
29	177.5	15.9	198	16	AA080781
30	177.5	15.9	198	16	AA080781
31	177.5	15.9	198	16	AA080781
32	177.5	15.9	198	16	AA080781
33	177.5	15.9	198	16	AA080781
34	177.5	15.9	198	16	AA080781
35	177.5	15.9	198	16	AA080781
36	177.5	15.9	198	16	AA080781
37	177.5	15.9	198	16	AA080781
38	177.5	15.9	198	16	AA080781
39	177.5	15.9	198	16	AA080781
40	177.5	15.9	198	16	AA080781
41	177.5	15.9	198	16	AA080781
42	177.5	15.9	198	16	AA080781
43	177.5	15.9	198	16	AA080781
44	177.5	15.9	198	16	AA080781
45	177.5	15.9	198	16	AA080781

ALIGNMENTS

RESULT 1

AAB18636

ID AAB18636 standard; Protein; 210 AA.

XX AAB18636;

XX 22-JAN-2001 (first entry)

XX Amino acid sequence of murine fibroblast growth factor (FGF)-21.

XX pD10-VEGFuc; gene delivery vector; eye disease; neovascular disease;
XX neurotrophic factor; anti-angiogenic factor; eye disease; glaucoma;
XX macular degeneration; diabetic retinopathy; retinitis pigmentosa;
XX inherited retinal degeneration; surgery-induced retinopathy;
XX retinal detachment; photic retinopathy; toxic retinopathy;
XX trauma-induced retinopathy; wet age related macular degeneration;
XX ARMD; retinopathy; fibroblast growth factor-20; FGF-20.

XX Mus sp.

XX WO200054813-A2.

XX 21-SEP-2000.

XX 15-MAR-2000; 2000WO-US07062.

XX 15-MAR-1999; 99US-0124460.

XX 06-JAN-2000; 2000US-0174984.

XX (CHIR) CHIRON CORP.

XX (REGC) UNIV CALIFORNIA.

XX Manning WC, Dwarki VJ, Rendahl K, Zhou S, McGee LH, Lau D;

XX Flannery JG, Miller S, Wang F, Di Polo A;

XX

```
XX WPI: 2000-618862/59.
DR N-PSDB: AAA75631.
XX
XX Treating or preventing eye diseases or inhibiting neovascular disease
PT of the eye, comprises intraocularly administering a gene delivery
PT vector that directs expression of neurotrophic factors or
PT anti-angiogenic factors -
XX
XX Disclousure: Fig 30; 86pp; English.
XX
XX The present sequence represents a murine fibroblast growth factor (FGF)
CC -21. FGF-20 is expressed using a gene delivery vector of the invention.
CC Vectors of the invention are used for treating or preventing eye
CC diseases, or inhibiting neovascular disease of the eye. The gene
CC delivery vector directs the expression of one or more neurotrophic
CC factors, or anti-angiogenic factors, such that the disease of the eye
CC is prevented or treated. The gene delivery vectors are useful for
CC treating or preventing diseases of the eye such as macular degeneration,
CC diabetic retinopathy, inherited retinal degeneration such as retinitis
CC pigmentosa, glaucoma, surgery-induced retinopathy, retinal detachment,
CC photic retinopathy, toxic retinopathy or trauma-induced retinopathy and
CC for inhibiting neovascular diseases such as wet age related macular
CC degeneration (ARM) or retinopathy of prematurity.
XX
XX Sequence 210 AA;
SQ
Query Match 100.0%; Score 1115; DB 21; Length 210;
Best Local Similarity 100.0%; Pred. No. 4.8e-102;
Matches 210; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MEWMSRVCTGLGWRLLLAVLLGVQAYPIPDSSPLLQFGQVQRQRYLYTDDDDQTEA 60
DB 1 mewmrsrvctglwrlilavllgvaypdpssplllqfggvrqrylytdddqdeca 60
QY 61 HLEIRDTGVVGAHRSPELSLELKALPGVITQILGVKASRFLCQPDGALYSGSPHFDP 120
DB 61 hleiredgtvgaahrspeleslelkalkpgvitiqilgvkasrfllcqpdpdgalysphfdpe 120
QY 121 ACSFRELLEDGYNVYQSEAHGLPLRLPKOKDSFNQDQATSWGPVRLPMLPGLLHEPDQAG 180
DB 121 acsfrelliedgynvyqseahglpirlpkdpsnqdatwgpvrilpmpgllhepqdqag 180
QY 181 FLPPPEPDVGSSDPLSMVEPLQGRSPSYAS 210
DB 181 flppeppdvvgssdplsmveplqgrspsyas 210
RESULT 2
ID AAB73069 standard; Protein; 153 AA.
XX
XX AAB73069;
XX
XX 17-MAY-2001 (first entry)
XX
XX Human fibroblast growth factor 19 homologue FGF19X.
XX
XX Human; fibroblast growth factor 19; FGF19X; embryonic development;
KW proliferative disorder; cancer; restenosis; psoriasis;
KW rheumatoid arthritis; Dupuytren's contracture.
XX
XX Homo sapiens.
XX
XX WO200118209-A1.
XX
XX 15-MAR-2001.
XX
XX 08-SEP-2000; 2000WO-US24863.
XX
XX 10-SEP-1999; 99US-0153303.
XX
XX 03-APR-2000; 2000US-0194246.
```

```
PR 19-JUL-2000; 2000US-0619251.
XX (CURA-) CURAGEN CORP.
XX
XX Shimkets RA, Vernet C, Burgess C, Fernandes E, Taupier R;
PI Quinn KE, Spyteck KA, Rastelli L, Herrmann JL;
XX
XX WPI: 2001-218559/22.
DR N-PSDB: AAF76715.
XX
XX Fibroblast growth factor-19X polypeptides and polynucleotides useful
PT for diagnosis, prevention, treatment of proliferative, differentiative,
PT tumorigenic disorders such as tumor, psoriasis, rheumatoid arthritis -
XX
XX Claim 11; Page 7; 97pp; English.
XX
XX The present invention describes the protein and coding sequences of the
CC human fibroblast growth factor (FGF) 19 homologue FGF19X, the former of
CC which is shown here. The sequences can be used in the prognosis and
CC treatment of proliferative diseases such as cancer, restenosis,
CC psoriasis, rheumatoid arthritis and Dupuytren's contracture, as well as
CC to stimulate cell growth for treating neurological disorders such as
CC Alzheimer's disease.
XX
XX Sequence 153 AA;
SQ
Query Match 54.1%; Score 603.5; DB 22; Length 153;
Best Local Similarity 86.9%; Pred. No. 7.7e-52;
Matches 119; Conservative 5; Mismatches 12; Indels 1; Gaps 1;
QY 12 GLWVRLLLAVLLGVQAYPIPDSSPLLQFGQVQRQRYLYTDDDDQTEAHLEIREDTGVV 71
DB 12 glwvs-vlagillgacqahpdpssplllqfggvrqrylytddaqteahleiredgtvg 70
QY 72 GAAHRSPELSLELKALPGVITQILGVKASRFLCQPDGALYSGSPHFDPACSFRELLED 131
DB 71 gaadqspesllqalkpgvitiqilgvksrflcqpdpdgalyslhfdpeacsfrellled 130
QY 132 GYNVYQSEAHGLPLRLP 148
DB 131 gynvyqseahglplhlp 147
RESULT 3
ID AAY08583 standard; Protein; 216 AA.
XX
XX AAY08583;
XX
XX 05-AUG-1999 (first entry)
XX
XX Human PRO533 protein fragment.
XX
XX PRO533; FGF-19; fibroblast growth factor; human; diagnosis; treatment;
KW tumour; neoplastic cell growth; cell proliferation; tumorigenesis; cancer;
KW autocrine signalling.
XX
XX Homo sapiens.
XX
XX WO9927100-A1.
XX
XX 03-JUN-1999.
XX
XX 25-NOV-1998; 98WO-US25190.
XX
XX 21-SEP-1998; 98US-0158432.
XX
XX 25-NOV-1997; 97US-0066840.
XX
XX (GETH ) GENENTECH INC.
XX
XX Botstein D, Goddard A, Gurney AL, Hillan KJ, Lawrence DA;
PI Roy MA;
```


WPI; 1999-229532/19.
N-PsDB; AAX28430.

Antibodies against specific proteins overexpressed in tumours

Example 1; Fig 6; 130pp; English.

This sequence represents the FGF-8 homologue PRO5533.

The invention relates to antibodies (Ab) that bind to any of the polypeptides (I) Designated PRO187; PRO533; PRO214; PRO240; PRO211; PRO330; PRO261; PRO246 or EBAF-2. The Ab, or other agents that inhibit expression and/or activity of (I) are used: (i) to inhibit growth of tumours; and (ii) as diagnostic/prognostic reagents for detection or quantification of (I) in cells or tissues, by standard immunoassays, with overexpression being indicative of cancer. For therapeutic use, the Ab may be conjugated to a toxin, chemotherapeutic agent or radioisotope. Genes expressing (I), many of which are growth factor homologues, are overexpressed in some cases of cancer.

Sequence 216 AA;

Query Match 23.5%; Score 262.5; DB 20; Length 216;
Best Local Similarity 34.7%; Pred. No. 4.8e-18;
Matches 75; Conservative 33; Mismatches 95; Indels 13; Gaps 8;

QY 4 MSRSVTGLGVRLLLAVFLGTVQAYPIPDSPLLQF--GGVQRVRYLYTDDQQD-TEA 60
Db 1 mrsgcvvvhw-i-laglwavagrplafsdaghvhvgwgdpirirhlvtsephglssc 58
 :||| : ||| : |::| : |::| : |::| : |::| :
QY 61 HLEIRDEGTIVGAHRSPESLLELKALKPGVIQLIGKASRFILCQPDPGNALYCSPHFDFE 120
Db 59 flriradgvdvcargqshslleikavalrtvaikghsvrylcmgadgkmgdgllysee 118
 :||| : ||| : |::|::|: :||| : ||| : ||| : ||| :
QY 121 ACSEFRELLEDGYNVYGSEAHGLPLRLPQ-KDSPNQDATSGVP-RFLPM-PGLLHEPQD 177
Db 119 dcfaeeirlpdgvnyvrsekhrflpsvlssakqrlyknrgfllpnlfmlpmvppeeped 178

QY 178 QAGFLPPE----PPDVGSDDLFWVEPLQG-RPSPY 208
Db 179 lrghlesdmffspldetdsmdpfglvltgleavrpspf 214

RESULT 6
AAB33434
ID AAB33434 standard; Protein; 216 AA.
XX AAC
AC AAB33434;
XX DT
DT 29-JAN-2001 (first entry)
XX Human PRO533 protein UNQ334 SEQ ID NO:112.
DE Human; immune related disease; diagnosis; antinflammatory; cardiant;
KW dermatological; antiarthritic; antirheumatic; immunosuppressive;
KW haemstatic; antithyroid; antidabetic; nootropic; neuroprotective;
KW antianemic; hepatotropic; virucide; antipsoriatic; antiallergic;
KW antiasthmatic; systemic lupus erythematosus; rheumatoid arthritis;
KW osteoarthritis; spondylarthropathy; systemic sclerosis; sarcoidosis;
KW idiopathic inflammatory myopathy; Sjogren's syndrome; thyroiditis;
KW systemic vasculitis; autoimmune haemolytic anaemia; diabetes mellitus;
KW autoimmune thrombocytopaenia; immune-mediated renal disease;
KW demyelinating disease; hepatobiliary disease; Whipple's disease;
KW inflammatory bowel disease; gluten-sensitive enteropathy;
KW autoimmune disease; immune-mediated skin disease; allergic disease;
KW immunological disease; transplantation associated disease;
KW graft rejection; graft-versus-host-disease.
OS Homo sapiens.
XX XQ
PN WQ200053758-A2.
XX XX

CC acid encoding the antibodies are used in the production of the
CC antibodies. The antibodies and nucleic acids encoding them are used for
CC diagnosing a tumour in a mammal. The antibodies are used for inhibiting
CC the growth of tumour cells and identifying compounds that inhibit a
CC biological or immunological activity of and/or expression of a PRO187,
CC PRO533, PRO214, PRO240, PRO211, PRO230, PRO261, PRO246 or PRO317
CC polypeptide. The antibody can be used in antibody dependent enzyme
CC mediated prodrug therapy (ADEPT) by conjugating the antibody to a
CC prodrug-activating enzyme which converts a prodrug to an anti-cancer
CC drug. The antibodies can be fluorescently labelled and monitored by light
CC microscopy, flow cytometry or fluorimetry for diagnosis and prognosis of
CC tumours.
XX
SQ Sequence 216 AA;

Query Match 23.5%; Score 262.5; DB 21; Length 216;
Best Local Similarity 34.7%; Pred. No. 4.8e-18;
Matches 75; Conservative 33; Mismatches 95; Indels 13; Gaps 8;
QY 4 MRSRVGTGLWVRLAVFLGVLGYQAYPIPDSSPLLQF--GGQVRORYLYTDDQD-TEA 60
Db 1 mrsqcvvhwvi--laglwlavagrplafsdagphvnygwdpirlrhlytsghglssc 58
QY 61 HLEIREDTGVGAHRSPELLEKALKPGVIOILGVKASRFLCQPDGALYGSHPFDPE 120
Db 59 flriradgvdvcargqsahsleikavalrtvaikghsvrylcmgadmkgmgllysee 118
QY 121 ACSFRELLLEDGYNVQSEAHGLPLRLPQ-KDSPNQDATSWGPV-RFLPW-PGLLHEPQD 177
Db 119 dcafeeiirpdgynvyvrysekhrlpvsalsakqrlgkngfipshfplmlpmvpeeped 178
QY 178 QAGFLPPE---PPDVGSSDPLSMVEPLQG-RSPSY 208
Db 179 lrglhlesdmfsspletddmpfgivtgleavrspsf 214

RESULT 8
AAB68593
ID AAB68593 standard; Protein; 216 AA.
XX
AC AAB68593;
DT 27-APR-2001 (first entry)
XX
DE PRO533.
XX
KW Cytostatic; PRO protein; tumour; cancer.
XX
OS Homo sapiens.
XX
PN WO200105836-A1.
XX
PD 25-JAN-2001.
XX
PF 20-DEC-1999; 99WO-US30999.
XX
PR 20-JUL-1999; 99US-0144758.
PR 26-JUL-1999; 99US-0145698.
PR 08-SEP-1999; 99WO-US20594.
PR 13-SEP-1999; 99WO-US20594.
PR 15-SEP-1999; 99WO-US21090.
PR 05-OCT-1999; 99WO-US23089.
PR 29-NOV-1999; 99WO-US28214.
PR 30-NOV-1999; 99WO-US28313.
PR 02-DEC-1999; 99WO-US28564.
XX
PA (GETH) GENENTECH INC.
XX
PI Botstein D, Goddard A, Gurney AL, Hillan KJ, Roy MA, Wood WI;
XX WPI; 2001-091968/10.
DR N-PSDB; AAF58498.

XX New antibody that binds to a PRO polypeptide, e.g. PRO187 and PRO533,
PT useful for diagnosing and treating cancers -
XX
XX Claim 61; Fig 4; 196pp; English.
XX
CC The present invention relates to PRO proteins and coding sequences. The
CC present sequence is one such PRO protein. It was found that the PRO genes
CC are amplified in the genome of tumour cells. The gene amplification is
CC expected to be associated with the overexpression of the gene product and
CC contributes to tumorigenesis. Therefore, antagonists of PRO proteins are
CC useful for the treatment of benign or malignant tumours, leukaemias,
CC lymphoid malignancies and other disorders such as neuronal, glial,
CC astrocytal, hypothalamic, glandular, epithelial, inflammatory and
CC immunologic disorders.
XX
SQ Sequence 216 AA;

Query Match 23.5%; Score 262.5; DB 22; Length 216;
Best Local Similarity 34.7%; Pred. No. 4.8e-18;
Matches 75; Conservative 33; Mismatches 95; Indels 13; Gaps 8;
QY 4 MRSRVGTGLWVRLAVFLGVLGYQAYPIPDSSPLLQF--GGQVRORYLYTDDQD-TEA 60
Db 1 mrsqcvvhwvi--laglwlavagrplafsdagphvnygwdpirlrhlytsghglssc 58
QY 61 HLEIREDTGVGAHRSPELLEKALKPGVIOILGVKASRFLCQPDGALYGSHPFDPE 120
Db 59 flriradgvdvcargqsahsleikavalrtvaikghsvrylcmgadmkgmgllysee 118
QY 121 ACSFRELLLEDGYNVQSEAHGLPLRLPQ-KDSPNQDATSWGPV-RFLPW-PGLLHEPQD 177
Db 119 dcafeeiirpdgynvyvrysekhrlpvsalsakqrlgkngfipshfplmlpmvpeeped 178
QY 178 QAGFLPPE---PPDVGSSDPLSMVEPLQG-RSPSY 208
Db 179 lrglhlesdmfsspletddmpfgivtgleavrspsf 214

RESULT 9
AAB31201
ID AAB31201 standard; Protein; 216 AA.
XX
AC AAB31201;
XX
DT 20-APR-2001 (first entry)
XX
DE Amino acid sequence of human polypeptide PRO553.
XX
KW Human; secreted protein; transmembrane protein; PRO196; PRO444; PRO183;
KW PRO185; PRO210; PRO215; PRO217; PRO242; PRO288; PRO365; PRO1361; PRO1308;
KW PRO1183; PRO1272; PRO1419; PRO4999; PRO7170; PRO248; PRO353; PRO1318;
KW PRO1600; PRO9940; PRO533; PRO301; PRO187; PRO337; PRO1411; PRO4356;
KW PRO246; PRO265; PRO941; PRO10096; PRO6003; PRO6004; PRO350; PRO2630;
KW PRO6309; cell death; genetic disorder; transgenic animal; gene therapy.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
XX Peptide 1..22
FT /note= "signal peptide"
FT Modified-site 15..21
FT /note= "N-myristoylation site"
FT Binding-site 48..59
FT /note= "prokaryotic membrane lipoprotein lipid attachment site"
FT Modified-site 54..60
FT /note= "N-myristoylation site"
FT Modified-site 66..72
FT /note= "N-myristoylation site"
FT Modified-site 78..82
FT /note= "casein kinase II phosphorylation site"

QY 129 LEDGYNVYQS-EAHLPLRLPKDQSPNQDATSWGVRFLPMPGLLHEPDQD----- 178
Db 120 lengdyvvhspqyhf-----vslgrakrafipgmpppsqflsrneip 165

QY 179 -AGFLPPEP-----PDVGSDDLMSVPELQGRSPSYAS 210
Db 166 lhfntpplrthrtsaeddserdpnlvklprarmtpapas 205

RESULT 14
AAB73070
ID AAB73070 standard; Protein; 142 AA.
AC AAB73070;
XX 17-MAY-2001 (first entry)
DT Human fibroblast growth factor 19 fragment.
DE Human; fibroblast growth factor 19; FGF19X; embryonic development;
XX proliferative disorder; cancer; restenosis; psoriasis;
KW rheumatoid arthritis; Dupuytren's contracture.
OS Homo sapiens.
XX WO200118209-A1.
XX 15-MAR-2001.
XX 08-SEP-2000; 2000WO-US24863.
XX 10-SEP-1999; 99US-0153303.
PR 03-APR-2000; 2000US-0194246.
PR 19-JUL-2000; 2000US-0619251.
XX (CURA-) CURAGEN CORP.
XX ShmKets RA, Vernet C, Burgess C, Fernandes E, Taupier R;
PI Quinn KE, Spyteck KA, Rastelli L, Herrmann JL;
XX WPI; 2001-218559/22.
XX Fibroblast growth factor-19X polypeptides and polynucleotides useful
PT for diagnosis, prevention, treatment of proliferative, differentiative,
PT tumorigenic disorders such as tumor, psoriasis, rheumatoid arthritis -
XX Disclosure; Page 8; 97pp; English.
PS The present invention describes the protein and coding sequences of the
CC human fibroblast growth factor (FGF) 19 homologue FGF19X. The sequences
CC can be used in the prognosis and treatment of proliferative diseases such
CC as cancer, restenosis, psoriasis, rheumatoid arthritis and Dupuytren's
CC contracture, as well as to stimulate cell growth for treating
CC neurological disorders such as Alzheimer's disease.
XX Sequence 142 AA;
SQ

Query Match 18.6%; Score 207.5; DB 22; Length 142;
Best Local Similarity 36.2%; Pred. No. 7.le-13;
Matches 50; Conservative 23; Mismatches 60; Indels 5; Gaps 3;

QY 13 LWRVLLAVFLGVQAYPIPDSSPLLOF--GGVRRORYLYTDDDDQD-TEAHLETRDGT 69
Db 1 vwi--laglwavagrpafsdagphvgygdprlrhltytsphglsscfllradgv 58

QY 70 VVGAHRSPESLLELKALPGVQIQLGVKASRFLCQQPDGALYGSFHPDPEACSFRELL 129
Db 59 vdcargqgaahsilleikavaltvtalkghsvrylcmgagdkmqgillqyseedcafeeeir 118

QY 130 EDGYNVYQSEAHGLPLRL 147
XX . j|||||:| | | | |

Db 119 pdgynvyvyrsekhrlpvsl 136

RESULT 15
AAY08582
ID AAY08582 standard; Protein; 213 AA.
AC AAY08582;
XX 05-AUG-1999 (first entry)
DT Human FGF-15 protein fragment.
DE PRO533; FGF-19; fibroblast growth factor; human; diagnosis; treatment;
XX tumour; neoplastic cell growth; cell proliferation; tumorigenesis; cancer;
KW autocrine signalling; FGF-15.
XX Homo sapiens.
OS WO9927100-A1.
XX 03-JUN-1999.
XX 25-NOV-1998; 98WO-US25190.
XX 21-SEP-1998; 98US-0158432.
PR 25-NOV-1997; 97US-0066840.
XX (GETH) GENENTECH INC.
XX Botstein D, Goddard A, Gurney AL, Hillan KJ, Lawrence DA;
PI Roy MA;
XX WPI; 1999-347718/29.
XX Nucleic acid encoding fibroblast growth factor - 19, useful for the
PT diagnosis, prevention and treatment of cancers
PT Disclosure; Fig 3; 88pp; English.
PS This invention describes a novel human fibroblast growth factor, PRO533,
CC also known as fibroblast growth factor-19 (FGF-19). The nucleic acids,
CC methods and PRO533 polypeptides disclosed may be used in the diagnosis
CC and treatment of tumours and/or conditions characterized by modulation of
CC PRO533 expression, or in the preparation of compositions for such
CC therapies. These compositions and methods may be used in the diagnosis
CC and treatment of neoplastic cell growth and proliferation in mammals
CC (especially humans). The invention is based on the identification of
CC genes that are amplified in the genome of tumour cells. Such gene
CC amplification is expected to be associated with the over expression of
CC the gene product and contribute to tumourgenesis and/or autocrine
CC signalling. Accordingly, the proteins encoded by the amplified genes are
CC believed to be useful targets for the diagnosis and/or treatment of
CC certain cancers and may act as predictors of the prognosis for tumour
CC treatments.
XX Sequence 213 AA;
SQ

Query Match 18.6%; Score 207.5; DB 20; Length 213;
Best Local Similarity 31.6%; Pred. No. 1.2e-12;
Matches 66; Conservative 30; Mismatches 90; Indels 23; Gaps 8;

QY 17 LLAVFLGV-----YQAYPIPDSSPLLOFG-GQV-RORYLYTDDDDQDTEAHLETRDG 68
Db 9 lviatlwavsgprlaqqsqsvsdedplflygwkitrlylsagpyvsnclfrirsdg 68

QY 69 TVVGAHRSPESLLELKALPGVQIQLGVKASRFLCQQPDGALYGSFHPDPEACSFRELL 128
Db 69 svdceedqnmrllefravalktkidvssvrylcmgsadgkiylirysedctfreem 128

QY 129 LEDGYNVYQSEAHGLPLRLPKDQSPNQDATSWGVRFLPMPGLLHEPDQAG-----F 181
XX . |||||:| | | | |

Db 129 dclgynyqysmkhhlhifiqa-kpreqlqdqkpsnfip---vfhrsffetgdqlrskmf 184
Qy 182 LPPEPPDVGSDDLPLSMVEPLQG--RSPSY 208
Db 185 slplesd--smdpfrmvedvdlvkpsf 211

Search completed: August 6, 2001, 20:57:49
Job time: 9721 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 6, 2001, 22:37:53 ; Search time 2566.06 Seconds
(without alignments)
3912.056 Million cell updates/sec

Title: US-09-391-861-3

Perfect score: 649
Sequence: 1 atgaatgatgagatctag.....ctgactcttctctaactta 649

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1344157 segs, 773874588 residues

Total number of hits satisfying chosen parameters: 2688314

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl:*
1: gb_ba1:*
2: gb_ba2:*
3: gb_ba3:*
4: gb_in1:*
5: gb_in2:*
6: gb_in3:*
7: gb_cm:*
8: gb_ov:*
9: gb_pat1:*
10: gb_pat2:*
11: gb_ph:*
12: gb_p11:*
13: gb_p12:*
14: gb_p13:*
15: gb_p14:*
16: em_ba1:*
17: em_ba2:*
18: em_fun:*
19: em_hgo_hum:*
20: em_hgo_inv:*
21: em_hgo_rod:*
22: em_htg_hum1:*
23: em_htg_hum2:*
24: em_htg_hum3:*
25: em_htg_hum4:*
26: em_htg_hum5:*
27: em_htg_hum6:*
28: em_htg_hum7:*
29: em_htg_hum8:*
30: em_htg_inv1:*
31: em_htg_inv2:*
32: em_htg_other:*
33: em_htg_rod:*
34: em_hum1:*
35: em_hum2:*
36: em_hum3:*
37: em_hum4:*
38: em_hum5:*
39: em_hum6:*
40: em_hum7:*
41: em_in:*
42: em_cm:*
43: em_or:*

44: em_ov:*
45: em_pat:*
46: em_ph:*
47: em_p1:*
48: em_ro:*
49: em_sts:*
50: em_sy:*
51: em_un:*
52: em_v1:*
53: gb_sts1:*
54: gb_sts2:*
55: gb_sts3:*
56: gb_sy:*
57: gb_un:*
58: gb_v11:*
59: gb_v12:*
60: gb_htg1:*
61: gb_htg2:*
62: gb_htg3:*
63: gb_htg4:*
64: gb_htg5:*
65: gb_htg6:*
66: gb_htg7:*
67: gb_htg8:*
68: gb_htg9:*
69: gb_htg10:*
70: gb_htg11:*
71: gb_htg12:*
72: gb_htg13:*
73: gb_htg14:*
74: gb_htg15:*
75: gb_htg16:*
76: gb_htg17:*
77: gb_htg18:*
78: gb_htg19:*
79: gb_htg20:*
80: gb_htg21:*
81: gb_htg22:*
82: gb_htg23:*
83: gb_htg24:*
84: gb_htg25:*
85: gb_pr1:*
86: gb_pr2:*
87: gb_pr3:*
88: gb_pr4:*
89: gb_pr5:*
90: gb_pr6:*
91: gb_pr7:*
92: gb_pr8:*
93: gb_pr9:*
94: gb_rol:*
95: gb_rol2:*
96: gb_in4:*
97: gb_pr10:*
98: em_ba3:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	633	97.5	633	94	AB025718 Mus muscu
2	400.2	61.7	630	85	AB021975 Homo sapi
3	297.4	45.8	215734	75	AC073828 Mus muscu
4	296.6	45.7	9257	94	AF214655 Mus muscu
5	283.8	43.7	514	10	AX097639 Sequence
6	197.2	30.4	179538	68	AC024740 Homo sapi
7	195.6	30.1	110000	60	AC008749 Homo sapi
8	195.6	30.1	110000	60	AC008749_1 Continuation (2 of

C 9	194	29.9	4033	85	AB006136	Homo sapi
C 10	194	29.9	37402	87	AC009002	Homo sapi
C 11	135.2	20.8	227949	70	AC026803	Homo sapi
C 12	68.4	10.5	756	85	AB037973	Homo sapi
C 13	68.4	10.5	1612	89	AF263537	Homo sapi
C 14	57.8	8.9	756	94	AB037889	Homo sapi
C 15	57.8	8.9	1559	94	AF263536	Mus muscu
C 16	54.2	8.4	651	85	AB018122	Homo sapi
C 17	54.2	8.4	2137	10	AX076894	Homo sapi
C 18	54.2	8.4	2137	10	AX076894	Homo sapi
C 19	54.2	8.4	2137	10	AX076894	Homo sapi
C 20	47.8	7.4	2291	8	AF110400	Homo sapi
C 21	43.8	6.7	1824	94	AF007268	Mus muscu
C 22	42.4	6.5	676	12	AF115191	Phaseolus
C 23	42.4	6.5	676	12	AF115191	Phaseolus
C 24	41.4	6.4	677	12	AF115200	Phaseolus
C 25	40.6	6.3	161903	67	AC021996	Homo sapi
C 26	40.6	6.3	166620	68	AC024612	Homo sapi
C 27	40.6	6.3	173765	88	AC022007	Homo sapi
C 28	40.6	6.3	173793	60	AC007783	Homo sapi
C 29	40.6	6.3	191834	69	AC026196	Homo sapi
C 30	40.6	6.3	197360	65	AC018829	Homo sapi
C 31	40.6	6.3	216905	87	AC018809	Homo sapi
C 32	39.4	6.1	11048	92	HS889J22B	Human DNA
C 33	39.4	6.1	155622	84	HS889J22	Human DNA
C 34	38.4	5.9	139290	73	AC068096	Homo sapi
C 35	37.6	5.8	190394	76	AC079886	Rattus no
C 36	37.4	5.7	116441	79	AL162257	Homo sapi
C 37	37.2	5.7	126141	80	AL356300	Homo sapi
C 38	37.2	5.7	184467	74	AC073241	Homo sapi
C 39	37.2	5.7	2426	10	I05274	Sequence 2
C 40	37	5.7	2426	10	I05274	Sequence 1
C 41	37	5.7	2426	10	I05274	Sequence 1
C 42	37	5.7	3398	93	HSEKRP	X02158 Human gene
C 43	37	5.7	3401	10	I08406	Sequence 1
C 44	37	5.7	110195	79	AL162741	Homo sapi
C 45	36.8	5.7	196003	76	AC079419	Mus muscu

ALIGNMENTS

RESULT 1	AB025718	633 bp	mRNA	11-Jul-2000
LOCUS	AB025718	Mus musculus mRNA for FGF-21, complete cds.		
ACCESSION	AB025718.1	GI:9049446		
VERSION	AB025718.1	GI:9049446		
KEYWORDS	FGF-21.			
SOURCE	Mus musculus	CDNA to mRNA.		
ORGANISM	Mus musculus			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
AUTHORS	1 (sites)			
TITLE	Nishimura,T., Nakatake,Y., Konishi,M. and Itoh,N.			
JOURNLT	Identification of a novel FGF, FGF-21, preferentially expressed in the liver(1)			
MEDLINE	Biochim. Biophys. Acta 1492 (1), 203-206 (2000)			
REFERENCE	2 (bases 1 to 633)			
AUTHORS	Itoh,N.			
JOURNLT	Submitted (02-APR-1999) to the DDBJ/EMBL/Genbank databases			
REFERENCE	Nobuyuki Itoh, Kyoto University, Graduate School of Pharmaceutical Sciences, Department of Genetic Biochemistry; Yoshida-Shimodachi, Sakyo, Kyoto, Kyoto 606-8501, Japan			
FEATURES	(E-mail:itohnobu@pharm.kyoto-u.ac.jp, Tel:81-75-753-4540, Fax:81-75-753-4600)			
SOURCE	Location/Qualifiers			
gene	1..633			
	/organism="Mus musculus"			
	/db_xref="taxon:10090"			
	1..633			

CDS

/gene="FGF-21"

1..633

/gene="FGF-21"

/codon_start=1

/product="FGF-21"

/protein_id="BA099416.1"

/db_xref="GI:9049447"

/translation="MEMMSRYGTGLVIRLLAVELLGVQAVIPDPSPLQFGGQVQRIYTDODTDAHLERPDGVNVAARSPSLLEIKLRPGDSFNQATSRICQDPGALYGSFHFDEPACSFRELLLEDGVNYSSEHGLPLRPKDSFNQATSRGVRLPMPGLHPEPDQAGFLPPPPVSSDPLSNVEPLQGRSPSTAS"

BASE COUNT 136 a 198 c 173 g 126 t

ORIGIN

Query Match 97.5%; Score 633; DB 94; Length 633;

Best Local Similarity 100.0%; Pred. No. 6,2e-147;

Matches 633; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	atggaatgagtagaatcagatcagaaggttgggaacccctgggaactgtgtggctcgaacgtcgtgtgct	60
DB	1	ATGGAAATGAGTAGATCAGATTGTTGGAGCCCTGGGACTGTGGTCCGACTGCTGCTGCT	60
QY	61	gtctctcgtcgtggtggtcttaacaagatacccatccctgactcagccccctctcag	120
DB	61	GTCCTCCTGCTGGGGGTCTACCAAGCATACCCATCTGATCTCAGCCCCCTCTCAG	120
QY	121	tttgagggttaagtcgagcagaggttacctctaacagatgagaccaaagactgaagc	180
DB	121	TTTGGGGTGAATCGCGGAGAGTACCTCTACAGATGAGACCAACACACTGAAGCC	180
QY	181	caactgagagatcagagagatgtagaacagtgtgtagggcagacaccgcagtcagaagt	240
DB	181	CACCTGAGATCAGGAGATGAGAGATGAGATGAGATGAGATGAGATGAGATGAGAT	240
QY	241	ctctcgtgagatcaaacgcttgaagcagaggtgtaattcaatcctggtgtgtaagcctct	300
DB	241	CTCTCGAGATCAAAAGCTTGAAGCAGAGGTGTAATCAATCCTGGGTGTCAAAAGCCTCT	300
QY	301	agggtctcttggcaaacagcagatgtagctctctatggtatgctcacttgaatcctgag	360
DB	301	AGGTTCTTGGCCAAAGCAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGAT	360
QY	361	gacctgagcttcagagaacagctgctgtagagagcgtgtacaatgtgtacagctgaagcc	420
DB	361	GCCTGACGCTTCAGAGAACTGCTGCTGAGAGAGCGTTAAATGTGTACCAAGTCTGAAGCC	420
QY	421	catggcctgccccctgctgctcctcagaaagagatccccaacacagatgcaacatcctgg	480
DB	421	CATGGCCTGCCCTGCGTCTGCTCAGAAAGAGATCCCAACACAGATGCAACATCTCTGG	480
QY	481	gtagcgtgtgagctctctgcccacatgcaagcgtgtctcaagagagcccaagacagagga	540
DB	481	GGAGCTGTGGCTTCTGCTGCCATGAGGCGTGTCTCAAGAGGCCCAACACAGAGGA	540
QY	541	ttctctgccccagagccccagatgtgggtcctcctgacccccctgagcattgtagagcct	600
DB	541	TTCTCTGCCCCAGAGCCCCAAGATGTGGGCTCTCTGACCCCTTAGCATGTGATAGGCT	600
QY	601	ttacaggagccgaagccccagctatgctgtcga 633	
DB	601	TTACAGGAGCCGAAGCCCCAGCTATGCTGTCTGA 633	
RESULT 2			
AB021975	AB021975	630 bp	mRNA
LOCUS	AB021975	Homo sapiens mRNA for FGF-21, complete cds.	PRI
DEFINITION	AB021975		03-AUG-2000
ACCESSION	AB021975.1	GI:9049444	
VERSION	AB021975.1	GI:9049444	
KEYWORDS	new FGF.		
SOURCE	Homo sapiens cDNA to mRNA.		
ORGANISM	Homo sapiens		

[illegible]

Oy	533	aagcaggattccgcgcccccaagaaccccagatgttgcttcctctgaaccctcgactgg	532
Dd	530	CACCCGGAATCTCGGCCCCCAGACCCTCCGGATGTGGGCTCCTCGSACCCTTGAGCATGG	589
Oy	593	tagagccttacagggccgaagccccagcatgatgcgtccta	633
Dd	590	TGGGACTTCCCAAGGGCCGAAAGCCCAAGCTACGCTTCCTGA	630
RESULT	3		
AC073828			
LOCUS			
DEFINITION	AC073828 215734 bp DNA HTG 29-JUN-2000 Mus musculus clone RP23-9J18, WORKING DRAFT SEQUENCE, 21 unordered pieces.		
AC073828			
VERSION	AC073828.1	GI:8810445	
KEYWORDS	HTG; HTGS_PHASE1; HTGS_DRAFT.		
SOURCE	Mus musculus house mouse.		
ORGANISM	Mus musculus		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.		
AUTHORS	1 (bases 1 to 215734)		
TITLE	DOE Joint Genome Institute.		
REFERENCE	Sequencing of Mouse Unpublished		
JOURNAL	2 (bases 1 to 215734)		
AUTHORS	DOE Joint Genome Institute.		
TITLE	Direct Submission		
JOURNAL	Submitted (29-JUN-2000) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA		
COMMENT	-----Genome Center Center: Joint Genome Institute Center Code: JGI Web site: http://www.jgi.doe.gov ----- Project Information Center Project Name: 1740562 Center clone name: RPCI-23_9J18 ----- Summary Statistics Consensus quality: 196667 bases at least Q40 Consensus quality: 207971 bases at least Q30 Consensus quality: 209928 bases at least Q20 Estimated insert size: 207740; agarose-fp estimation Quality coverage: 213734; sum-of-contigs estimation Quality coverage: 6.12 in Q20 bases; agarose-fp estimation NOTE: This is a 'working draft' sequence. It currently consists of 21 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as * runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved. 1 1013: contig of 1013 bp in length 1014 1113: gap of unknown length 1114 2175: contig of 1062 bp in length 2176 2275: gap of unknown length 2276 3429: contig of 1154 bp in length 3430 3529: gap of unknown length 3530 4884: contig of 1355 bp in length 4885 4984: gap of unknown length 4985 6848: gap of 1864 bp in length 6849 9317: gap of 2369 bp in length 9318 9417: gap of unknown length 9418 12128: contig of 2711 bp in length 12129 12228: gap of unknown length 12229 14970: contig of 2742 bp in length 14971 15070: gap of unknown length 15071 19571: contig of 4501 bp in length		

```

* 19572 19671: gap of unknown length
* 19672 25961: contig of 6290 bp in length
* 25962 26061: gap of unknown length
* 26062 36753: contig of 10692 bp in length
* 36754 36853: gap of unknown length
* 36854 49116: contig of 12263 bp in length
* 49117 49216: gap of unknown length
* 49217 61879: contig of 12663 bp in length
* 61880 61979: gap of unknown length
* 61980 72513: contig of 10534 bp in length
* 72514 72613: gap of unknown length
* 72614 83721: contig of 11108 bp in length
* 83722 83821: gap of unknown length
* 83822 98633: contig of 14812 bp in length
* 98634 98733: gap of unknown length
* 98734 118323: contig of 19590 bp in length
* 118324 118423: gap of unknown length
* 118424 137668: contig of 19245 bp in length
* 137669 162338: contig of 24570 bp in length
* 162339 162438: gap of unknown length
* 162439 186625: contig of 24187 bp in length
* 186626 186725: gap of unknown length
* 186726 215734: contig of 29009 bp in length.

```

Location/Qualifiers

```

1. 215734
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone="RP23-9J18"

```

BASE COUNT 54325 a 53055 c 52767 g 53583 t 2004 others

ORIGIN

```

Query Match 45.8%; Score 297.4; DB 75; Length 215734;
Best Local Similarity 99.7%; Pred. No. 3.9e-64;
Matches 298; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 342 gccctacattgactcctgagcctcagctcagaggaactcgtctgtaggaagcgtttacaa 401
Db 136527 GCCTCATTGATCTGAGGCGCTGAGCTTCAAGAACTGCTGAGAGGAGCGGTACAA 136586

QY 402 tgtgtaccagctcgtgaagccatgagcctcgtcgtctgctcagaaggaactcccaaa 461
Db 136587 TGTGTACCAAGCTGGAAGCCATGGCGCTGCGCTGCTGCTCAAGAAAGACTCCCAAA 136646

QY 462 ccaggaatgcaaatcctcgtggaactcgtgcttctcctccatgccaagcctgctccaca 521
Db 136647 CCAGGATGCAACATCTGGGAGCCTGTGCGCTTCTGCCATGCCAGGCTGCTCCACGA 136706

QY 522 gccccaagaacaaagagattcctgccccagagccccagatgtaggtccctctgaccc 581
Db 136707 GCCCAAGAACCAAGAGATTCTGCCCCAGAGCCCCCAAGATGTGGGCTCTCTGACCC 136766

QY 582 cctgagcattgtagagcctttacagggccgaagccccagctatgcgtcctgactcttc 640
Db 136767 CCTGAGCATGTGTAGACCTTTACAGGGCCCAAGCCCAAGCTATGCGTCTGACTCTTCC 136825

```

RESULT 4
AF214655/c
LOCUS AF214655 9257 bp DNA ROD 23-MAR-2000
DEFINITION Mus musculus alpha(1,2)fucosyltransferase FUT1 (Fut1) gene.
ACCESSION AF214655
VERSION AF214655.1 GI:7288502
KEYWORDS
SOURCE house mouse.
ORGANISM Mus musculus.
Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 9257)
AUTHORS Domino, S.E. and Lowe, J.B.

```

TITLE Mus musculus alpha(1,2)fucosyltransferase FUT1 genomic sequence
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 9257)
AUTHORS Domino, S.E. and Lowe, J.B.
TITLE Direct Submission
JOURNAL Submitted (13-DEC-1999) HHMI, University of Michigan, 1150 W. Med.
Ctr. Dr., Ann Arbor, MI 48109-0650, USA

FEATURES
source
1. 9257
/organism="Mus musculus"
/strain="129/Ola"
/db_xref="taxon:10090"
/chromosome="7"
/map="23.2: between K1k1 and Ldh3"
/cell_line="E14"
/cell_type="ES"
/gene="Fut1"
/product="alpha(1,2)fucosyltransferase FUT1"
<578..>6716
/gene="Fut1"
583..6716
/gene="Fut1"
/EC_number="2.4.1.69"
/note="glycosyltransferase: similar to the Mus musculus
strain ICR sequences deposited at GenBank Accession
Numbers Y09883 and AF113533; similar to the Mus musculus
strain NIH Swiss sequence deposited at GenBank Accession
Number U90553; similar to the Homo sapiens H blood group
alpha(1,2)fucosyltransferase FUT1 sequences deposited at
GenBank Accession Numbers M3531 and Z69587"
/codon_start=1
/product="alpha(1,2)fucosyltransferase FUT1"
/protein_id="AA045145.1"
/db_xref="GI:7288503"
/translation="MMPSPRRQLCTFLVLCVLSAGSPFFHLNGNFFRNLTSLVLC
SYHLKSPVAVVCLPPLDTGNSPSCPEQSSLSGTWITPGRGNOMGOVATLL
ALAOINGROAPTOPMHAALAPVRPIS.PVDIPVDSITPMOHLVLDMSREESHLE
DPFLKSGFPSCSWTFPHHLRQDIREPFLHHLHRLBGAQYLLSGIRIPAGIRPTEPG
VHVRGDLLEVAMPNFRKGVVDRAVLDQAMVFRARHDPLEVTYSNGMKMCNEDIT
SHGDVVEFGNGDEGTGKDFALVLCNMTINTIGTFFGMAVYLAGGDTVYLANETLPD
SEFLKIFRPEAAFLFEWGINADSLPIAOAPDPMKPSLFRV"
BASE COUNT 2267 a 2195 c 2580 g 2215 t

ORIGIN

Query Match 45.7%; Score 296.6; DB 94; Length 9257;
Best Local Similarity 98.7%; Pred. No. 1.2e-63;
Matches 299; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 342 gccctacattgactcctgagcctcagctcagagaactcgtcgtgtaggaagcgtttacaa 401
Db 1354 GCCTCATTGATCTGAGGCGCTGAGCTTCAAGAACTGCTGAGAGGAGCGGTACAA 1295

QY 402 tgtgtaccagctcgtgaagccatgagcctcgtcgtctgctcagaaggaactcccaaa 461
Db 1294 TGTGTACCAAGCTGGAAGCCCATGGCGCTGCGCTGCTGCTCAAGAAAGACTCCCAAA 1235

QY 462 ccaggaatgcaaatcctcgtggaactcgtgcttctcctccatgccaagcctgctccaca 521
Db 1234 CCAGGATGCAACATCTGGGAGCCTGTGCGCTTCTGCCATGCCAGGCTGCTCCACGA 1175

QY 522 gccccaagaacaaagagattcctgccccagagccccagatgtaggtccctctgaccc 581
Db 1174 GCCCAAGAACCAAGAGATTCTGCCCCAGAGCCCCCAAGATGTGGGCTCTCTGACCC 1115

QY 582 cctgagcattgtagagcctttacagggccgaagccccagctatgcgtcctgactcttc 641
Db 1114 CCTGAGCATGTGTAGACCTTTACAGGGCCCAAGCCCAAGCTATGCGTCTGACTCTTCC 1055

QY 642 tga 644

```



```
FEATURES
source
1. 179538
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="19"
/clone="RP11-801D6"
1. 1801
/misc_feature /note="assembly_name:Contig13"
1902. 4641
/misc_feature /note="assembly_name:Contig14"
4742. 9679
/misc_feature /note="assembly_name:Contig15"
9780. 13392
/misc_feature /note="assembly_name:Contig16"
13493. 17164
/misc_feature /note="assembly_name:Contig17"
17265. 21510
/misc_feature /note="assembly_name:Contig18"
21611. 27089
/misc_feature /note="assembly_name:Contig19"
27190. 35636
/misc_feature /note="assembly_name:Contig20"
35737. 45537
/misc_feature /note="assembly_name:Contig21"
45638. 56451
/misc_feature /note="assembly_name:Contig22"
56552. 66802
/misc_feature /note="assembly_name:Contig23"
66903. 79118
/misc_feature /note="assembly_name:Contig24"
79219. 94355
/misc_feature /note="assembly_name:Contig25"
94456. 111274
/misc_feature /note="assembly_name:Contig26"
111375. 130600
/misc_feature /note="assembly_name:Contig27"
130701. 150278
/misc_feature /note="assembly_name:Contig28
clone_end:SP6
vector_side:left"
150379. 179538
/misc_feature /note="assembly_name:Contig29"
42230 a 47023 c 46289 g 42392 t 1604 others
BASE COUNT
ORIGIN
Query Match 30.4% Score 197.2; DB 68; Length 179538;
Best Local Similarity 72.3%; Pred. No. 3.2e-39;
Matches 256; Conservative 0; Mismatches 98; Indels 0; Gaps 0;
OY 280 atccgggtgtcaaacgctcagttctcttcccaacagcagatgagactctctatgga 339
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 130126 ATCTGGGCTCTTACATCCAGGAAACAGAGAACCCCTGCTCTGTATCCGTTTGTCCCC 130185
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 340 tcgcctcatttgatcctgagcctgagcctcagacagactgctgctgagagactac 399
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 130186 TAGCTCCACTTTGACGAGCGCTGAGAGCTTCCGGAGAGCTTCTTGAGAGAGATAC 130245
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 400 aatgtgtacagcttgagcccatgctgctgctgctgctgctgctgctgagagactccca 459
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 130246 AATGTTTACAGTCCGAGCCAGGCGCTCCCGTGCACCTCCAGGGAACAAAGTCCCA 130305
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 460 aaccaggaatgaacatccctgggagcctgtgctcctgcccacagcagcctgtctcac 519
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
```

```
Db 130306 CACGGGAGACCTTCGACACCCGAGAGACAGCTGCTCTGTCGACACTACAGAGCCTGCCCCC 130365
OY 520 gagccccaagaccagcagatctctgcccagagcccccagatgtggtctctctac 579
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 130366 GCACCCCCGAGACCCACCCGGAATCTGGGCCCCCAGCCCCCGAGATGAGCTCTCGGAC 130425
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 580 cccctgagcatgttagagccttcaagagcgaagcccaagctatgctcctga 633
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 130426 CCTCTGAGCATGTGTGGACCTTCCAGGGCCGAGACCCAGCTATGCTTCCGA 130479
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 7
AC008749.0/c
WPCOMMENT
Sequence split into 5 fragments LOCUS AC008749 Accession AC008749
Fragment Name Begin End
AC008749_0 1 110000
AC008749_1 100001 210000
AC008749_2 200001 310000
AC008749_3 300001 410000
AC008749_4 400001 467420
LOCUS AC008749 467420 bp DNA HTG 21-JUN-2000
DEFINITION Homo sapiens chromosome 19 clone CTD-2611012, WORKING DRAFT
SEQUENCE, 127 unordered pieces.
ACCESSION AC008749
VERSION AC008749.5 GI:8575912
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 467420)
DOE Joint Genome Institute.
Unpublished
2 (bases 1 to 467420)
DOE Joint Genome Institute.
Direct Submission
Submitted (03-AUG-1999) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
On Jun 21, 2000 this sequence version replaced gi:7689801.
-----Genome Center
Center: Joint Genome Institute
Center Code: JGI
Web site: http://www.jgi.doe.gov
-----
Project Information
Center Project Name: 832953, BC797977
Center clone name: CITB-EL_2611012
-----
Summary Statistics
Consensus quality: 353446 bases at least Q40
Consensus quality: 412781 bases at least Q30
Consensus quality: 426617 bases at least Q20
Estimated insert size: 454820; agarose-gel estimation
Quality coverage: 9.78 in Q20 bases; agarose-gel estimation
Quality coverage: 3.25 in Q20 bases; sum-of-coverage estimation.
NOTE: This is a 'working draft' sequence. It currently
* consists of 127 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
1 1208: contig of 1208 bp in length
* 1209 1308: gap of unknown length
* 1309 2441: contig of 1133 bp in length
* 2442 2541: gap of unknown length
* 2542 3647: contig of 1106 bp in length
* 3648 4788: gap of unknown length
* 4788: contig of 1041 bp in length
```


* 4789 4888: gap of unknown length
* 4889 6132: contig of 1244 bp in length
* 6133 6232: gap of unknown length
* 6233 7544: contig of 1312 bp in length
* 7545 7644: gap of unknown length
* 7645 8892: contig of 1248 bp in length
* 8893 8992: gap of unknown length
* 8993 10296: contig of 1304 bp in length
* 10297 10397: gap of unknown length
* 10397 11725: contig of 1329 bp in length
* 11726 11825: gap of unknown length
* 11826 13734: contig of 1909 bp in length
* 13735 13834: gap of unknown length
* 13835 15056: contig of 1222 bp in length
* 15057 15156: gap of unknown length
* 15157 16358: contig of 1202 bp in length
* 16359 16458: gap of unknown length
* 16459 17875: contig of 1417 bp in length
* 17876 17975: gap of unknown length
* 17976 19527: contig of 1552 bp in length
* 19528 19627: gap of unknown length
* 19628 21424: contig of 1797 bp in length
* 21425 21524: gap of unknown length
* 21525 22793: contig of 1269 bp in length
* 22794 22893: gap of unknown length
* 22894 23905: contig of 1012 bp in length
* 23906 24005: gap of unknown length
* 24006 25440: contig of 1435 bp in length
* 25441 25540: gap of unknown length
* 25541 26895: contig of 1355 bp in length
* 26896 26995: gap of unknown length
* 26996 28178: contig of 1183 bp in length
* 28179 28278: gap of unknown length
* 28279 29887: contig of 1609 bp in length
* 29888 29987: gap of unknown length
* 29988 31869: contig of 1882 bp in length
* 31870 31969: gap of unknown length
* 31970 33535: contig of 1566 bp in length
* 33536 33635: gap of unknown length
* 33636 34963: contig of 1328 bp in length
* 34964 35063: gap of unknown length
* 35064 36881: contig of 1818 bp in length
* 36882 36981: gap of unknown length
* 36982 38148: contig of 1167 bp in length
* 38149 38248: gap of unknown length
* 38249 39889: contig of 1641 bp in length
* 39890 39989: gap of unknown length
* 39990 41963: contig of 1974 bp in length
* 41964 42063: gap of unknown length
* 42064 43733: contig of 1670 bp in length
* 43734 43833: gap of unknown length
* 43834 45414: contig of 1581 bp in length
* 45415 45514: gap of unknown length
* 45515 47046: contig of 1532 bp in length
* 47047 47146: gap of unknown length
* 47147 48965: contig of 1819 bp in length
* 48966 49065: gap of unknown length
* 49066 51369: contig of 2304 bp in length
* 51370 51469: gap of unknown length
* 51470 53128: contig of 1659 bp in length
* 53129 53228: gap of unknown length
* 53229 54580: contig of 1252 bp in length
* 54481 54580: gap of unknown length
* 54581 56485: contig of 1905 bp in length
* 56486 56585: gap of unknown length
* 56586 58664: contig of 2079 bp in length
* 58665 58764: gap of unknown length
* 58765 59959: contig of 1195 bp in length
* 59960 60059: gap of unknown length
* 60060 62303: contig of 2244 bp in length
* 62304 62403: gap of unknown length
* 62404 64204: contig of 1801 bp in length
* 64205 64304: gap of unknown length

* 64305 66196: contig of 1892 bp in length
* 66197 66296: gap of unknown length
* 66297 67878: contig of 1582 bp in length
* 67879 67978: gap of unknown length
* 67979 69965: contig of 1987 bp in length
* 69966 70065: gap of unknown length
* 70066 71633: contig of 1568 bp in length
* 71634 71734: gap of unknown length
* 71734 73978: contig of 2245 bp in length
* 73979 74078: gap of unknown length
* 74079 76073: contig of 1995 bp in length
* 76074 76173: gap of unknown length
* 76174 78469: contig of 2296 bp in length
* 78470 78569: gap of unknown length
* 78570 81250: contig of 2681 bp in length
* 81251 81350: gap of unknown length
* 81351 83762: contig of 2412 bp in length
* 83763 83862: gap of unknown length
* 83863 85889: contig of 2127 bp in length
* 85890 86089: gap of unknown length
* 86090 88156: contig of 2067 bp in length
* 88157 88256: gap of unknown length
* 88257 90318: contig of 2062 bp in length
* 90319 90418: gap of unknown length
* 90419 92289: contig of 1871 bp in length
* 92290 92389: gap of unknown length
* 92390 95174: contig of 2785 bp in length
* 95175 95274: gap of unknown length
* 95275 98333: contig of 3059 bp in length
* 98334 98433: gap of unknown length
* 98434 99975: contig of 1542 bp in length
* 99976 100075: gap of unknown length
* 100076 101499: contig of 1424 bp in length
* 101500 101599: gap of unknown length
* 101600 103848: contig of 2249 bp in length
* 103849 103948: gap of unknown length
* 103949 106127: contig of 2179 bp in length
* 106128 106227: gap of unknown length
* 106228 108402: contig of 2175 bp in length
* 108403 108502: gap of unknown length
* 108503 110948: contig of 2446 bp in length
* 110949 111048: gap of unknown length
* 111049 113905: contig of 2857 bp in length
* 113906 114005: gap of unknown length
* 114006 117256: contig of 3251 bp in length
* 117257 117356: gap of unknown length
* 117357 119135: contig of 1779 bp in length
* 119136 119235: gap of unknown length
* 119236 121325: contig of 2090 bp in length
* 121326 121425: gap of unknown length
* 121426 123954: contig of 2529 bp in length
* 123955 124054: gap of unknown length
* 124055 126851: contig of 2797 bp in length
* 126852 126951: gap of unknown length
* 126952 129652: contig of 2701 bp in length
* 129653 129752: gap of unknown length
* 129753 132233: contig of 2481 bp in length
* 132234 132333: gap of unknown length
* 132334 135268: contig of 2935 bp in length
* 135269 135368: gap of unknown length
* 135369 137746: contig of 2378 bp in length
* 137747 137846: gap of unknown length
* 137847 141549: contig of 3703 bp in length
* 141550 141649: gap of unknown length
* 141650 144391: contig of 2742 bp in length
* 144392 144491: gap of unknown length
* 144492 147414: contig of 2923 bp in length

Query Match 30.1%; Score 195.6; DB 60; Length 110000;
Best Local Similarity 72.0%; Pred. No. 8; 8e-39;
Matches 255; Conservative 0; Mismatches 99; Indels 0; Gaps 0;
OY 280 atccctgggtcacaagcctctagttcttctgcacacagccagatgagctctctatgga 339

```

|||||
Db 109817 ATCTGGGCTTACATACAGAAACAGAGAACCTGTCTCTGATCCCTTTTGTCCCC 109758
OY 340 tcgctcaatttgatcctgagcctgctcagagaaactgctgagagaggttac 399
Db 109757 TAGCTCCACTTTGACCCCTGAGGCGCTTCCGGAGAGCTGCTTCTTGAGAGAGATAC 109698
OY 400 aatgtgtacagctcgtgaagcccaatgctgcccctgctgctgctcagaaagactccca 459
Db 109697 AATGTTTACAGTCCGAGCCACGCGCTCCCGCTGACCTGACAGGAGAACAGTCCCA 109638
OY 460 aaccagagtgaaacatctctgaggactgtgcttctcctcagccagagcctctccac 519
Db 109637 CACCGGGACCTGACACCCCGAGGACACCTGCTTCTGACACAGGCGCTGCCCC 109578
OY 530 gagccccaagccaagcagagatctcctgccccagagccccaagatgtgagctctctgac 579
Db 109577 GCACCCCGGAGCCACCGGAGATCTGCCCCCAGGCCCGGATGTGGCTCTCTCGGAC 109518
OY 580 cccctgagcatgtgtagagcctttagaagggccgaagccccaagctatgctctga 633
Db 109517 CCTGTGACATGTGTGGAGACTTCCACGAGGCGGAGCCACCTACGCTTCTCTGA 109464

```

RESULT 8 AC008749_1/c

Sequence split into 5 fragments LOCUS AC008749 Accession AC008749

Fragment Name	Begin	End
AC008749_0	1	110000
AC008749_1	100001	210000
AC008749_2	200001	310000
AC008749_3	300001	410000
AC008749_4	400001	467420

Continuation (2 of 5) of AC008749 from base 100001 (AC008749 Homo sapiens chromosome 19

Query Match Best Local Similarity 30.1%; Score 195.6; DB 60; Length 110000; Pred. No. 8.8e-39; Matches 255; Conservative 0; Mismatches 99; Indels 0; Gaps 0;

```

OY 280 atctcgggtgtcaagcctctagttctcttgcacaagccagatgagctctatgga 339
Db 9817 ATCTGGGCTTACATACAGAAACAGAGAACCTGTCTCTGATCCCTTTTGTCCCC 9758
OY 340 tcgctcaatttgatcctgagcctgctcagagaaactgctgagagaggttac 399
Db 9757 TAGCTCCACTTTGACCCCTGAGGCGCTTCCGGAGAGCTGCTTCTTGAGAGAGATAC 9698
OY 400 aatgtgtacagctcgtgaagcccaatgctgcccctgctgctgctcagaaagactccca 459
Db 9697 AATGTTTACAGTCCGAGCCACGCGCTCCCGCTGACCTGACAGGAGAACAGTCCCA 9638
OY 460 aaccagatgaaacatctctgaggactgtgcttctcctcagccagagcctctccac 519
Db 9637 CACCGGGACCTGACACCCCGAGGACACCTGCTTCTGACACAGGCGCTGCCCC 9578
OY 520 gagccccaagccaagcagagatctcctgccccagagccccaagatgtgagctctctgac 579
Db 9577 GCACCCCGGAGCCACCGGAGATCTGCCCCCAGGCCCGGATGTGGCTCTCTCGGAC 9518
OY 580 cccctgagcatgtgtagagcctttagaagggccgaagccccaagctatgctctga 633
Db 9517 CCTGTGACATGTGTGGAGACTTCCACAGGCGGAGCCACCTACGCTTCTCTGA 9464

```

RESULT 9
AB006136/c
LOCUS AB006136 4033 bp DNA PRI 20-JUL-2000
DEFINITION Homo sapiens gene for alpha 1,2-fucosyltransferase, 5' flanking
region and partial cds.
ACCESSION AB006136
VERSION AB006136.1 GI:3242453

KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
REFERENCE
TITLES
JOURNAL
COMMENT
FEATURES
source

FUT1, alpha (1, 2) fucosyltransferase.
 Homo sapiens peripheral leukocytes DNA.
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (sites)
 Koda, Y., Soejima, M. and Kimura, H.
 Changing transcription start sites in H-type
 alpha(1,2)fucosyltransferase gene (FUT1) during differentiation of
 the human erythroid lineage
 Eur. J. Biochem. 256 (2), 379-387 (1998)
 98430978
 2 (bases 1 to 4033)
 Koda, Y.
 Direct Submission
 Submitted (04-AUG-1997) to the DDBJ/EMBL/GenBank databases. Yoshio
 Koda, Kurume University, School of Medicine, Department of Forensic
 Medicine; Asahimachi 67, Kurume, Fukuoka 830-0011, Japan
 (E-mail: ykoda@med.kurume-u.ac.jp, Tel: 81-942-31-7554,
 Fax: 81-942-31-7700)
 On Jun 20, 1998 this sequence version replaced gi:2317262.
 Sequence updated (16-Jun-1998).
 Location/Qualifiers
 1..4033
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /chromosome="19"
 /map="19q13.3"
 /rname="FUT1"
 /rsize_type="peripheral leukocytes"
 1..510
 /gene="FUT1"
 /number=1
 511..578
 /gene="FUT1"
 511..578
 /gene="FUT1"
 /standard_name="alpha(1,2)fucosyltransferase"
 /codon_start=1
 /product="FUT1"
 /protein_id="BA28952.1"
 /db_xref="GI:3242454"
 /translation="MGFHHVQAGLEILITSGDLPAWY"
 BASE COUNT 877 a 1242 c 1099 g 815 t
 ORIGIN

Query Match Best Local Similarity 29.9%; Score 194; DB 85; Length 4033; Pred. No. 4.5e-38; Matches 254; Conservative 0; Mismatches 100; Indels 0; Gaps 0;

```

OY 280 atctcgggtgtcaagcctctagttctcttgcacaagccagatgagcctctatgga 339
Db 1593 ATCTGGGCTTACATACAGAAACAGAGAACCTGTCTCTGATCCCTTTTGTCCCC 1534
OY 340 tcgctcaatttgatcctgagcctgctcagagaaactgctgagagaggttac 399
Db 1533 TAGCTCCACTTTGACCCCTGAGGCGCTTCCGGAGAGCTGCTTCTTGAGAGAGATAC 1474
OY 400 aatgtgtacagctcgtgaagcccaatgctgcccctgctgctgctcagaaagactccca 459
Db 1473 AATGTTTACAGTCCGAGCCACGCGCTCCCGCTGACCTGACAGGAGAACAGTCCCA 1414
OY 460 aaccagatgaaacatctctgaggactgtgcttctcctcagccagagcctctccac 519
Db 1413 CACCGGGACCTGACACCCCGAGGACACCTGCTTCTGACACAGGCGCTGCCCC 1354
OY 520 gagccccaagccaagcagagatctcctgccccagagccccaagatgtgagctctctgac 579
Db 1353 GCACCCCGGAGCCACCGGAGATCTGCCCCCAGGCCCGGATGTGGCTCTCTCGGAC 1294
OY 580 cccctgagcatgtgtagagcctttagaagggccgaagccccaagctatgctctga 633

```

Db 1293 CCTGTGAGCATGTGGAGACCTTCCAGGCGCGAAGCCCGAGCTACGCTTCTCTA 1240

RESULT 10
AC009002/c 37402 bp DNA PRI 13-AUG-2000
LOCUS Homo sapiens chromosome 19 clone L1NLR-279G3, complete sequence.
DEFINITION AC009002
ACCESSION AC009002.5 GI:9799769
VERSION HTG.
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 37402)
AUTHORS DOE Joint Genome Institute and Stanford Human Genome Center.
TITLE Direct Submission
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 37402)
AUTHORS DOE Joint Genome Institute.
TITLE Direct Submission
JOURNAL Submitted (03-AUG-1999) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
REFERENCE 3 (bases 1 to 37402)
AUTHORS DOE Joint Genome Institute and Stanford Human Genome Center.
TITLE Direct Submission
JOURNAL Submitted (13-AUG-2000) DOE Joint Genome Institute, 2800 Mitchell
Drive, Walnut Creek, CA 94598, USA
COMMENT On Aug 13, 2000 this sequence version replaced gi:9256105.
Draft Sequence Produced by DOE Joint Genome Institute
www.jgi.doe.gov
Finishing Completed at Stanford Human Genome Center
www.shgc.stanford.edu
Quality: Phrap Quality >=40 99.9% of Sequence;
Estimated Total Number of Errors is 0.
STS Content:
SHGC-35310 G28569.
FEATURES
Location/Qualifiers
source 1..37402
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="19"
/clone="L1NLR-279G3"
BASE COUNT 8189 a 9990 c 10374 g 8849 t
ORIGIN

Query Match 29.9%; Score 194; DB 87; Length 37402;
Best Local Similarity 71.8%; Pred. No. 2.8e-38;
Matches 254; Conservative 0; Mismatches 100; Indels 0; Gaps 0;

QY 280 atcctgggtgtcaagcctctagttcttgcacaagcagatgagctctctatga 339
|||||
Db 10061 ATCCTGGGTGTTCATCAGAAAACAGAGAACCTGTCTCTATCTCTTTTGTGCC 10002
|||||

QY 340 tcgacctacttgcctctgagcctcagctcagctcagaagactgctgttgaagcagttac 399
|||||
Db 10001 TACCTCACCATTGACCTGAGGCTGACGCTCCGGAGAGCTCTTGTGAGCGATAC 9942
|||||

QY 400 aatggtaccagctgaagcccaatgctgcctcctcgtctcgtcctcagaagaactccca 459
|||||
Db 9941 AATGTTTACAGTCCGAAGCCGACGGCTCCGCTGCTCACCCTGCAAGCAAGTCCCA 9882
|||||

QY 460 aaccagatcacatcctctgagactgtgcgtctcctcccatgcaagcctgcctcac 519
|||||
Db 9881 CACCGGAGACCTTCACCCGAGAGACCAAGCTCGTTCTCTGCTACTACCAAGCCTGCCCCC 9822
|||||

QY 520 gagccccaagacaagcagatctctgcctcccaagcctcccaagatgtggctcctcag 579
|||||
Db 9821 GCACCTCCGAGAGCCACCGCAATCTGCGCCCGCCCGCCGATGTGGGCTCCTCGGAC 9762
|||||

QY 580 cccctagcatgttagagccttaagggccgaagcccaagctatgctcctga 633
|||||

Db 9761 CCTGTGAGCATGTGGAGACCTTCCAGGCGCGAAGCCCGAGCTACGCTTCTCTA 9708

RESULT 11
AC026803/c 227949 bp DNA HTG 18-JUL-2000
LOCUS Homo sapiens chromosome 19 clone CTD-2639E6, WORKING DRAFT
DEFINITION AC026803
ACCESSION AC026803
VERSION AC026803.4 GI:9256691
KEYWORDS HTG; HTGS_PHASE2; HTGS_DRAFT.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 227949)
AUTHORS DOE Joint Genome Institute.
TITLE Sequencing of Human Chromosome 19
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 227949)
AUTHORS DOE Joint Genome Institute.
TITLE Direct Submission
JOURNAL Submitted (24-MAR-2000) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
COMMENT On Jul 18, 2000 this sequence version replaced gi:8576168.
-----Genome Center
Center: Joint Genome Institute
Center Code: JGI
Web site: http://www.jgi.doe.gov

Project Information
Center Project Name: 843459, BC808483
Center clone name: CITB-EL_2639E6

Summary Statistics
Consensus quality: 217198 bases at least Q40
Consensus quality: 224116 bases at least Q30
Consensus quality: 225875 bases at least Q20
Estimated insert size: 226670; agarose-fp estimation
Quality coverage: 6.85 in Q20 bases; agarose-fp estimation
Quality coverage: 6.83 in Q20 bases; sum-of-contigs estimation
NOTE: This is a 'working draft' sequence. It currently
* consists of 13 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* been provided by the submitter.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.

1 21840: contig of 21840 bp in length
1 21841: gap of unknown length
* 21941: 21940: gap of unknown length
* 31559: contig of 9619 bp in length
* 31560: 31559: gap of unknown length
* 31659: gap of unknown length
* 31660: 31659: gap of unknown length
* 36287: contig of 4528 bp in length
* 36288: 36287: gap of unknown length
* 59202: contig of 22915 bp in length
* 59203: 59202: gap of unknown length
* 59303: gap of unknown length
* 59304: 59303: contig of 9775 bp in length
* 69078: 69077: gap of unknown length
* 69177: 69078: contig of 11750 bp in length
* 80927: 80926: gap of unknown length
* 80928: 80927: gap of unknown length
* 81028: 81027: gap of unknown length
* 138192: 81028: contig of 57165 bp in length
* 138193: 138192: gap of unknown length
* 138293: 138193: gap of unknown length
* 160224: 138293: contig of 21932 bp in length
* 160325: 160224: gap of unknown length
* 161182: 160325: contig of 858 bp in length
* 161183: 161182: gap of unknown length
* 161283: 161183: gap of unknown length
* 162861: 161283: contig of 1579 bp in length
* 162862: 162861: gap of unknown length
* 162962: 162862: gap of unknown length
* 221619: 162962: contig of 58658 bp in length
* 221719: 221619: gap of unknown length

* 221720 225761: contig of 4042 bp in length
* 225762 225861: gap of unknown length
* 225862 227949: contig of 2088 bp in length.
Location/Qualifiers
1. .227949
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="19"
/clone="CTD-2639E6"
/clone_1bp="CalTech human BAC library D"

BASE COUNT 54671 a 58658 c 58905 g 54511 t 1204 others
ORIGIN

Query Match 20.8%; Score 135.2; DB 70; Length 227949;
Best Local Similarity 82.4%; Pred. No. 7.5e-24;
Matches 155; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

OY 53 tctctgctgtcttctgcttggtggtctacacagataccatccctgactccagccccc 112
|||||
Db 227632 TCGTGGCTGGTCTTCTGCTGGAGGCTCCAGGACACCCCATCCCTGACTCCAGTCTCTC 227573
|||||
OY 113 tctctcagtttggtggtcaagtcgcgcagaggtacacctacacagatgacgacccaagaca 172
|||||
Db 227572 TCCCTCAATTCGGGGGCCAAGTCCGGCAGCGGTACCTCTACACAGATGATGCCACGAGA 227513
|||||
OY 173 ctgaagccacactggagatcagggagatggaacagtggtgagcgacgacacccgcagtc 232
|||||
Db 227512 CAGAAGCCACCTGGAGATCAGGAGGATGGAGGTGGGGGGCGCTGACCAAGAGCC 227453
|||||
OY 233 cagaaagt 240
|||||
Db 227452 CCGAAGT 227445

RESULT 12
AB037973 756 bp mRNA PRI 11-NOV-2000
LOCUS AB037973 Homo sapiens FGF23 mRNA for FGF-23, complete cds.
ACCESSION AB037973
VERSION AB037973.1 GI:10119773
KEYWORDS
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS Yamashita,T., Yoshioka,M. and Itoh,N.
TITLE Identification of a novel fibroblast growth factor, FGF-23,
preferentially expressed in the ventrolateral thalamic nucleus of
the brain

JOURNAL Blochem. Biophys. Res. Commun. 277 (2), 494-498 (2000)

MEDLINE 20490027

REFERENCE 2 (bases 1 to 756)

AUTHORS Itoh,N.
TITLE Direct Submission
SUBMITTED (03-FEB-2000) to the DDBJ/EMBL/Genbank databases.
JOURNAL Nobuyuki Itoh, Kyoto University, Graduate School of Pharmaceutical
Sciences, Department of Genetic Biochemistry, Yoshida-Shimoadachi,
Sakyo, Kyoto, Kyoto 606-8501, Japan
(E-mail:itohnobu@pharm.kyoto-u.ac.jp, Tel:81-75-753-4540,
Fax:81-75-753-4600)

FEATURES
source Location/Qualifiers

1. .756
/organism="Homo sapiens"

gene /db_xref="taxon:9606"

1. .756
/gene="FGF23"

CDS 1. .756
/gene="FGF23"

1. .756
/codon_start=1

1. .756
/product="FGF-23"

1. .756
/protein_id="BAB13477.1"

/db_xref="GI:10119774"
/translation="MIGARIRLWVCAICSCVSMYLRAPVPAASPLGSSMGLILHYT
ATARNSHIQIKNGHVDGAPROTITYSKLMRSEDAQVVTITVMSRRYLQMDRNT
FGSHYEDDENCERFQHTLENGDYHSQYHFLVSLGAKRAFLPGMPPYSQFLSR
RNEIPLIHNTDPIRRHTRSAEDSDERPDVLVLRAMTPAPASCSOELPSADNSP
MASDPLGVVGRGVNTHAGTGTEGECRPFARFI"

BASE COUNT 159 a 250 c 212 g 135 t
ORIGIN

Query Match 10.5%; Score 68.4; DB 85; Length 756;
Best Local Similarity 53.8%; Pred. No. 1e-06;
Matches 141; Conservative 0; Mismatches 121; Indels 0; Gaps 0;

OY 180 ccaactggagatcagggagagatgtaacagtgtagcgcgacgaacccgcaagcgaag 239
|||||
Db 153 CCACCTGCAATCCACAGAGATGCCATGTGATGGCGACCCATCAGACCATCTACAG 212
|||||
OY 240 tctctgagatcgaagcccttgagccaggggtcatcgaatcccttggtgtcaagccctc 299
|||||
Db 213 TGCCCTGATCATCAGATCAGAGAGATGCTGCTTGTGTGATTTACAGTGTATGACGAG 272
|||||
OY 300 taagttctttgccaacagccagatgagctctctatgtatgcgctcacttgatctcta 359
|||||
Db 273 AAGATACCTCTGCATGATGATTTACAGAGCAACATTTTGGATCACACTATTTCACCCGGA 332
|||||
OY 360 ggcctgagcttcagaagactgctgtgagagcaggtttcaatggttaccagctcgaagc 419
|||||
Db 333 GAACCTGAGGTTCCAAACACAGAGAGAGCTGGAAGAGGAGTACAGCTTACACTCTCTCA 392
|||||
OY 420 ccaatgctgcccctgctgtc 441
|||||
Db 393 GTATCACTTCTGCTGATCTG 414

RESULT 13
AF263537 1612 bp mRNA PRI 14-DEC-2000
LOCUS AF263537 Homo sapiens FGF23 (FGF23) mRNA, complete cds.
ACCESSION AF263537
VERSION AF263537.1 GI:9964291
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS White,K.E., Evans,W.E., O'Riordan,J.L.H., Speer,M.C., Econs,M.J.,
Lorenz-Deptieux,B., Grabowski,M., Mellinger,T. and Strom,T.M.
TITLE Autosomal dominant hypophosphataemic rickets is associated with
mutations in FGF23

JOURNAL Nat. Genet. 26 (3), 345-348 (2000)

MEDLINE 20517346

REFERENCE 2 (bases 1 to 1612)

AUTHORS Strom,T.M.
TITLE Direct Submission
SUBMITTED (03-MAY-2000) Medizinische Genetik, Goethestr. 29,
Muenchen 80336, Germany

FEATURES
source Location/Qualifiers

1. .1612
/organism="Homo sapiens"

gene /db_xref="taxon:9606"

1. .1612
/map="12p13.3"

1. .1612
/clone="RPC111-338P6"

1. .1612
/gene="FGF23"

1. .1612
/codon_start=1

1. .1612
/product="FGF23"

1. .1612
/protein_id="AAG09917.1"

/db_xref="GI:9964292"
/translation="MLGARLRLVCAICVSCMSVLRAPYNASPLIGSSWGLIHLYT
ATARNSTYHLQIHKKHADVADPHOTIYSALMIRSEDAFVITGVMSRRYLCEMRGNI
FGSHYEDPENCERQHOTLENGYDYHSPQYHFLVSLGRAKRALPGMNPYQOPLSR
RNEIPLIHNTPIPRRHTRSADSESDERDPLNVLKPRARMPAPASCSQELPSADNSP
MASDPLGVGGGRVNTAGCGTGRGCRPRPKFI"
BASE COUNT 405 a 462 c 418 g 327 t
ORIGIN

Query Match 10.5%; Score 68.4; DB 89; Length 1612;
Best Local Similarity 53.8%; Pred. No. 8.6e-07;
Matches 141; Conservative 0; Mismatches 121; Indels 0; Gaps 0;

OY 180 ccacctgagatcaggagatggaacagtgtagcgccagcacaccgcaagcagaag 239
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 299 CCACCTGACATCCACAGATAGGCATGTGATGGCCACCATCAGACCATCTACAG 358
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 240 tctctgagctcaagccttggaagccagggtcaatcctcctgggtgtcaagcctc 299
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 339 TGCCCTGATGATCAGATCAGAGATGCTGCTTGTGTGATACAGGTGTGATGACAG 418
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 300 tagcttcttgccaacagccagatggagctctatgagatcgctcaacttgatcctga 359
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 419 AAGATACCTGTCATGATTCAGAGGCACATTTTGGATCACACTATTTCAGACCGGA 478
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 360 ggcctgcaagcttcagagaactgctgctggaagacgttacaatgtlaccagctgaagc 419
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 479 GAACCTGCGAGTTCCACACACCGACGTGAGAAACGGGTAGACAGCTTACCACTCTCTCA 538
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 420 ccattgctgctgcctgctgctg 441
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 539 GTATCACTCTCTGCTGATCTG 560
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 14
AB037889 756 bp mRNA ROD 11-NOV-2000
LOCUS
DEFINITION Mus musculus Fgf23 mRNA for FGF-23, complete cds.
ACCESSION AB037889
VERSION AB037889.1 GI:10119771
KEYWORDS
SOURCE Mus musculus cDNA to mRNA.
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 (sites)
AUTHORS Yamashita,T., Yoshioka,M. and Itoh,N.
TITLE Identification of a novel fibroblast growth factor, FGF-23,
preferentially expressed in the ventrolateral thalamic nucleus of
the brain.
JOURNAL Blochem. Biophys. Res. Commun. 277 (2), 494-498 (2000)
MEDLINE 20490027
REFERENCE 2 (bases 1 to 756)
AUTHORS Itoh,N.
TITLE Direct Submission
JOURNAL Submitted (31-JAN-2000) to the DDBJ/EMBL/GenBank databases.
Nobuyuki Itoh, Kyoto University, Graduate School of Pharmaceutical
Sciences, Department of Genetic Biochemistry; Yoshida-Shimoadachi,
Sakyo, Kyoto 606-8501, Japan
(E-mail:itohnobu@pharm.kyoto-u.ac.jp, Tel:81-75-753-4540,
Fax:81-75-753-4600)
FEATURES
source
1. 756
Location/Qualifiers
/organism="Mus musculus"
/db_xref="taxon:10090"
1. 756
/gene="Fgf23"
1. 756
/gene="FGF23"
1. 756
/codon_start=1
/product="FGF-23"
/protein_id="BAB13478.1"

/db_xref="GI:10119772"
/translation="MGCTLRILVYICVCSIGSTARAYPDTSPLIGSNMSLTHLYT
ATARNSTYHLQIHRDGVADTPIHOTIYSALMTTSEAGS VITGATRTFLCMDLHGNT
FGSLHSPENCERQHOTLENGYDYHSPQYHFLVSLGRAKRALPGMNPYQOPLSR
RNEIPLIHNTPIPRRHTRSADSESDERDPLNVLKPRARMPAPASCSQELPSADNSP
MASDPLGVGGGRVNTAGCGTGRGCRPRPKFI"
BASE COUNT 141 a 251 c 217 g 147 t
ORIGIN

Query Match 8.9%; Score 57.8; DB 94; Length 756;
Best Local Similarity 51.3%; Pred. No. 0.00044;
Matches 134; Conservative 0; Mismatches 127; Indels 0; Gaps 0;

OY 181 cactctgagatcaggagatggaacagtgtagcgccagcacaccgcaagcagaag 240
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 154 CCACCTGACATCCACAGATAGGCATGTGATGGCCACCATCAGACCATCTACAGT 213
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 241 ctctgagatcagaagccttggaagccagggtcaatcctcctgggtgtcaagcctc 300
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 214 GCCCTGATGATTCATCAGAGGACGCCGCTCTGTGTGATTAACAGGACCATGACTGA 273
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 301 aggttcttgccaacagccagatggagctctatgagatcgctcaacttgatcctga 360
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 274 AGGTTCTTGTATGATCTCCACGCAACATTTTGGATCGCTTACACTTCAGCCCAAG 333
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 361 gcttgagcttcagagaactgctgctggaagacgttacaatgtlaccagctgaagc 420
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 334 AATTGCAAGTTCGCCGACGTGAGAGTGGATGAGTACTACTTGTGCGCAGAG 393
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 421 catgctgccccctgctgctg 441
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 394 CATCACTACCTGCTGAGCCTG 414
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 15
AF263536 1559 bp mRNA ROD 14-DEC-2000
LOCUS
DEFINITION Mus musculus Fgf23 (Fgf23) mRNA, complete cds.
ACCESSION AF263536
VERSION AF263536.1 GI:9964289
KEYWORDS
SOURCE house mouse.
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 1559)
AUTHORS White,K.E., Evans,W.E., O'Riordan,J.L.H., Speer,M.C., Econs,M.J.,
Lorenz-Deplieux,B., Grabowski,M., Meltinger,T. and Strom,T.M.
TITLE Autosomal dominant hypophosphataemic rickets is associated with
mutations in FGF23
JOURNAL Nat. Genet. 26 (3), 345-348 (2000)
MEDLINE 20517346
REFERENCE 2 (bases 1 to 1559)
AUTHORS Strom,T.M.
TITLE Direct Submission
JOURNAL Submitted (03-MAY-2000) Medizinische Genetik, Goethestr. 29,
Muenchen 80336 Germany
FEATURES
source
1. 1559
Location/Qualifiers
/organism="Mus musculus"
/strain="BALB/c"
/db_xref="taxon:10090"
/chromosome="6"
/clone="Rp23-195E18"
/tissue_type="whole embryo"
1. 1559
/gene="Fgf23"
57. 812
/gene="Fgf23"
/codon_start=1
/product="FGF23"

